GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 29, 2004, 22:51:23 ; Search time 4429 Seconds
(without alignments)
2965.215 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 303
Sequence: 1 MGSGGDSLLGGRGSLPLLLL.....SGPRLPREARELRGQRRNTG 303

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Word size: 1

Total number of hits satisfying chosen parameters: 6934743

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	300	99.0	1346	6	BD074325	BD074325 50 human
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15	27	8.9	2886	10	AY277635	AY277635 Rattus no
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c 18	25	8.3	223269	2	AC120636	AC120636 Rattus no
19	25	8.3	250318	2	AC109983	AC109983 Rattus no
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c 21	10	3.3	1298	8	AK071342	AK071342 Oryza sat
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23	10	3.3	4437	10	MML1L	X94310 M.musculus
c 24	10	3.3	88098	9	AL451042	AL451042 Human DNA
c 25	10	3.3	123214	8	AP005191	AP005191 Oryza sat
26	10	3.3	162339	8	AC022457	AC022457 Oryza sat
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ALIGNMENTS

RESULT 1

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DEFINITION  50 human secreted proteins.
ACCESSION   BD074325
VERSION     BD074325.1  GI:22619928
KEYWORDS    JP 2001514024-A/30.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1346)
  AUTHORS   Moore,P.A., Ruben,S.M., Lafleur,D.W., Shi,Y., Rosen,C.A.,
            Olsen,H.S., Ebner,R. and Brewer,L.A.
  TITLE     50 human secreted proteins
  JOURNAL   Patent: JP 2001514024-A 30 11-SEP-2001;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001514024-A/30
            PD   11-SEP-2001
            PF   03-SEP-1998 JP 2000508394
            PR   05-SEP-1997 US    60/057626,05-SEP-1997 US    60/057663 PR
            05-SEP-1997 US    60/057669,12-SEP-1997 US    60/058667 PR
            12-SEP-1997 US    60/058974,12-SEP-1997 US    60/058973 PR
            12-SEP-1997 US    60/058666
            PI   PAUL A MOORE,STEVEN M RUBEN,DAVID W LAFLEUR,YANGGU SHI,CRAIG A

            PI   ROSEN,
            PI   HENRIK S OLSEN,REINHARD EBNER,LAURIE A BREWER PC
            C12N15/09,A61K38/00,A61K48/00,A61P17/02,A61P17/06,A61P19/00, PC
            A61P19/02,
            PC   A61P29/00,A61P31/04,A61P31/12,A61P35/00,C07K14/435,C07K16/18,
            PC   C12N1/15,
            PC
            C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/53,C12N15/ PC
             00,
            PC   A61K37/02,C12N5/00
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            CC   n equals a,t,g, or c
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FEATURES             Location/Qualifiers
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ORIGIN

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Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            99.01%          Indels:         0
DB:                     6               Gaps:           0

US-10-047-021-86 (1-303) x BD074325 (1-1346)

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Db         31 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 90

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
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Db         91 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCTTAGTCCACCCCCAGGAC 150

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
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Qy        121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
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Qy        141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
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Qy        181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer 200
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Qy        221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaVal 240
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Db        751 CGAATTCAGCTGGAAAATGTGACACTSCTGAACCCGGATCCTGCAGARGGCCCCAAGCCT 810

Qy        261 ArgProAlaValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThr 280
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Qy        281 ArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArgArg 300
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Qy        301 AsnThrGly 303
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RESULT 2
AX405719
LOCUS       AX405719                3267 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 134 from Patent WO0222660.
ACCESSION   AX405719
VERSION     AX405719.1  GI:21438877
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tang,Y.T., Liu,C., Zhou,P., Asundi,V., Zhang,J., Zhao,Q.A., Ren,F.,
            Xue,A.J., Yang,Y., Wehrman,T. and Drmanac,R.T.
  TITLE     Novel nucleic acids and polypeptides
  JOURNAL   Patent: WO 0222660-A 134 21-MAR-2002;
            HYSEQ, INC. (US)
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ORIGIN

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Percent Similarity:     98.51%          Conservative:   0
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Query Match:            48.84%          Indels:         4
DB:                     6               Gaps:           0

US-10-047-021-86 (1-303) x AX405719 (1-3267)

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Qy         60 oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
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Db        214 TCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACA 273

Qy         80 sHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
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Qy        120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140
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Db        394 TGGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCA 453

Qy        140 nIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPr 160
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Qy        160 oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLe 180
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Qy        180 uGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSe 200
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Qy        220 laAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaV 240
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Qy        240 alArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysP 260
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Qy        260 roArgProAlaValTrpLeu 266
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RESULT 3
AY358083
LOCUS       AY358083               3716 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA41404 magic roundabout (UNQ421) mRNA, partial
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ACCESSION   AY358083
VERSION     AY358083.1  GI:37181271
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3716)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
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            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 3716)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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                     PRPCLTPTPSEGSLANGWGSASEDNAASARASLVSSSDGSFLADAHFARALAVAVDSF
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ORIGIN

Alignment Scores:
Pred. No.:              4.37e-136       Length:         3716
Score:                  148.00          Matches:        261
Percent Similarity:     98.49%          Conservative:   0
Best Local Similarity:  98.49%          Mismatches:     2
Query Match:            48.84%          Indels:         4
DB:                     9               Gaps:           0

US-10-047-021-86 (1-303) x AY358083 (1-3716)

Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuIleMet 23
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Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
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Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
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Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
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Db        180 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 239

Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
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Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
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Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
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Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
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Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
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Db        480 CCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539

Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
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Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
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Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
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Db        659 TTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTC 718

Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
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Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
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Db        779 CGGTGTGGCTC 789

RESULT 4
AF361473
LOCUS       AF361473                3872 bp    mRNA    linear   PRI 15-NOV-2001
DEFINITION  Homo sapiens magic roundabout mRNA, complete cds.
ACCESSION   AF361473
VERSION     AF361473.1  GI:16930357
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3872)
  AUTHORS   Huminiecki,L. and Bicknell,R.
  TITLE     In silico cloning of novel endothelial-specific genes
  JOURNAL   Genome Res. 10 (11), 1796-1806 (2000)
  MEDLINE   20530916
   PUBMED   11076864
REFERENCE   2  (bases 1 to 3872)
  AUTHORS   Huminiecki,L. and Bicknell,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2001) ICRF, Institute of Molecular Medicine, John
            Radcliffe Hospital, Oxford OX3 9DS, UK
FEATURES             Location/Qualifiers
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                     /chromosome="11"
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                     EDAILKHRMDHSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWD
                     SRSPGVPLLPDTSTFYGSLIAELPSSTPARPSPQVPAVRRLPPQLAQLSSPCSSSDSL
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                     QSPGAVPQALVAWRALGPKLLSSSNELVTRHLPPAPLFPHETPPTQSQQTQPPVAPQA
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ORIGIN

Alignment Scores:
Pred. No.:              4.52e-136       Length:         3872
Score:                  148.00          Matches:        264
Percent Similarity:     98.51%          Conservative:   0
Best Local Similarity:  98.51%          Mismatches:     2
Query Match:            48.84%          Indels:         4
DB:                     9               Gaps:           0

US-10-047-021-86 (1-303) x AF361473 (1-3872)

Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
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Db        130 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 189

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
              |||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db        190 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACC 248

Qy         60 oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
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Db        249 TCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACA 308

Qy         80 sHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
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Qy        100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLe 120
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Qy        120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140
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Db        429 TGGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCA 488

Qy        140 nIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPr 160
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Db        489 GATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCC 548

Qy        160 oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLe 180
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Qy        180 uGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSe 200
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Qy        200 rAspGlu***-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgA 220
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Db        669 TGACGAAGG-GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCG 727

Qy        220 laAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaV 240
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Qy        260 roArgProAlaValTrpLeu 266
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Db        848 CTAGACCGGCGGTGTGGCTC 867
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RESULT 5
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LOCUS AX870164 756 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 5069 from Patent EP1074617.
ACCESSION AX870164
VERSION AX870164.1 GI:40025027
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesising full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 5069 07-FEB-2001;
Research Association for Biotechnology (JP)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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ORIGIN

Alignment Scores:

Pred. No.:	6.12e-109	Length:	756
Score:	120.00	Matches:	200
Percent Similarity:	98.04%	Conservative:	0
Best Local Similarity:	98.04%	Mismatches:	2
Query Match:	39.60%	Indels:	4
DB:	6	Gaps:	0

US-10-047-021-86 (1-303) x AX870164 (1-756)

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Db         40 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 99

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
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Db        100 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 159

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
              |||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db        160 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACC 218

Qy         60 oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
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Db        219 TCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACA 278

Qy         80 sHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 CCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCA 338

Qy        100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLe 120
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Db        339 CGATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCT 398

Qy        120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140
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Qy        140 nIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPr 160
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Db        578 TCCAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGA 637

Qy        200 erAspGlu 202
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Db        638 GTGACGAA 645
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RESULT 6
BD150226
LOCUS BD150226 756 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD150226
VERSION BD150226.1 GI:27855984
KEYWORDS JP 2002191363-A/5069.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 5069 09-JUL-2002;

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            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002191363-A/5069
            PD   09-JUL-2002
            PF   28-JUL-2000 JP 2000280990
            PI   TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
            PI   SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
             Primer for synthesizing full-length cDNA and use thereof FH   Key
                      Location/Qualifiers
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                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
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ORIGIN

Alignment Scores:
Pred. No.:              6.12e-109      Length:         756
Score:                  120.00         Matches:        200
Percent Similarity:     98.04%         Conservative:   0
Best Local Similarity:  98.04%         Mismatches:     2
Query Match:            39.60%         Indels:         4
DB:                     6              Gaps:           0

US-10-047-021-86 (1-303) x BD150226 (1-756)

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Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
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Db        100 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 159

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
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Db        160 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACC 218

Qy         60 oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
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Db        219 TCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACA 278

Qy         80 sHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
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Db        279 CCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCA 338

Qy        100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLe 120
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Db        339 CGATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCT 398

Qy        120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 TGGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCA 458

Qy        140 nIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPr 160
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Qy        160 oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGly-LysProLeuAlaL 180
              ||||||||||||||||||||||||||||||||||||||||    |||||||||||||||||
Db        519 GCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGA-GAAACCCCTGGCCC 577

Qy        180 euGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysS 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 TCCAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGA 637

Qy        200 erAspGlu 202
              ||||||||
Db        638 GTGACGAA 645

RESULT 7
AX883179
LOCUS       AX883179                4262 bp    DNA     linear   PAT 17-DEC-2003
DEFINITION  Sequence 18084 from Patent EP1074617.
ACCESSION   AX883179
VERSION     AX883179.1  GI:40038080
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primers for synthesising full-length cDNA and their use
  JOURNAL   Patent: EP 1074617-A 18084 07-FEB-2001;
            Research Association for Biotechnology (JP)
FEATURES              Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              2.65e-108      Length:         4262
Score:                  120.00         Matches:        263
Percent Similarity:     97.77%         Conservative:   0
Best Local Similarity:  97.77%         Mismatches:     3
Query Match:            39.60%         Indels:         6
DB:                     6              Gaps:           0

US-10-047-021-86 (1-303) x AX883179 (1-4262)

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RESULT 8
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DEFINITION Novel genes encoding protein kinase or protein phosphatase.
ACCESSION BD012213
VERSION BD012213.1 GI:22092402
KEYWORDS WO 0109345-A/11.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4262)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K., Otsuki,T., Funahashi,S., Seno,C. and Nezu,J.
TITLE Novel genes encoding protein kinase or protein phosphatase
JOURNAL Patent: WO 0109345-A 11 08-FEB-2001;
HELIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA, KOJI HAYASHI,KAORU SAITO,JUNICHI YAMAMOTO,SHIZUKO ISHII, OMOYASU SUGIYAMA, AI WAKAMATSU,KEIICHI NAGAI,TETSUJI OTSUKI,SHINICHI FUNAHASHI, HIAKI SENO, JUNICHI NEZU
COMMENT OS Homo sapiens (human)
PN WO 0109345-A/11
PD 08-FEB-2001
PF 28-JUL-2000 WO 2000JP005060
PR 29-JUL-1999 JP 99P 248036,11-JAN-2000 JP 00P 118776 PR 02-MAY-2000 JP 00P 183767,18-OCT-1999 US 60/159590 PR 17-FEB-2000 US 60/183322
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI, PI KAORU SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI,SHINICHI FUNAHASHI,CHIAKI SENO,
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FEATURES Location/Qualifiers
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ORIGIN

Alignment Scores:

Pred. No.:	2.65e-108	Length:	4262
Score:	120.00	Matches:	263
Percent Similarity:	97.77%	Conservative:	0
Best Local Similarity:	97.77%	Mismatches:	3
Query Match:	39.60%	Indels:	6
DB:	6	Gaps:	0

US-10-047-021-86 (1-303) x BD012213 (1-4262)

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RESULT 9
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LOCUS       BD160172                4262 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD160172
VERSION     BD160172.1  GI:27865930
KEYWORDS    JP 2002191363-A/15015.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4262)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 15015 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
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            PD   09-JUL-2002
            PF   28-JUL-2000 JP 2000280990
            PI   TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
            PI   SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI
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                     Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              2.65e-108      Length:         4262
Score:                  120.00         Matches:        263
Percent Similarity:     97.77%         Conservative:   0
Best Local Similarity:  97.77%         Mismatches:     3
Query Match:            39.60%         Indels:         6
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US-10-047-021-86 (1-303) x BD160172 (1-4262)

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Qy        260 ProArgProAlaValTrpLeu 266
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Db        817 CCTAGACCGGCGGTGTGGCTC 837

RESULT 10
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LOCUS       AK027852                4262 bp    mRNA    linear   PRI 01-AUG-2002
DEFINITION  Homo sapiens cDNA FLJ14946 fis, clone PLACE2000034, weakly similar
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ACCESSION   AK027852
VERSION     AK027852.1  GI:14042831
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
            Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H.,
            Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K.,
            Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
            Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 4262)
  AUTHORS   Isogai,T. and Otsuki,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology; cDNA library construction,
            5'- & 3'-end one pass sequencing and clone selection: Helix
            Research Institute (supported by Japan Key Technology Center etc.)
            and Department of Virology, Institute of Medical Science,
            University of Tokyo.
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ORIGIN

Alignment Scores:
Pred. No.:                2.65e-108      Length:          4262
Score:                    120.00         Matches:         263
Percent Similarity:       97.77%         Conservative:    0
Best Local Similarity:    97.77%         Mismatches:      3
Query Match:              39.60%         Indels:          6
DB:                       9              Gaps:            0

US-10-047-021-86 (1-303) x AK027852 (1-4262)

Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 99

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 159

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACC 218

Qy         60 oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 TCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACA 278

Qy         80 sHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 CCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCA 338

Qy        100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 CGATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCT 398

Qy        120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 TGGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCA 458

Qy        140 nIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 GATCCAGCCTCGAGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCC 518

Qy        160 oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGly-LysProLeuAlaL 180
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||
Db        519 GCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGA-GAAACCCCTGGCCC 577

Qy        180 euGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysS 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 TCCAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGA 637

Qy        200 erAspGlu***-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArg 219
              |||||||    ||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 GTGACGAAGG-GACCTACATGTGTGTGGCCACCAACAGCGCAGGACACAGGGAGAGCCGC 696

Qy        220 AlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAla 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        697 GCAGCCCGGGTTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCT 756

Qy        240 ValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLys 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 GTGCGAATTCAGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAG 816

Qy        260 ProArgProAlaValTrpLeu 266
              |||||||||||||||||||||
Db        817 CCTAGACCGGCGGTGTGGCTC 837

RESULT 11
BC014995
LOCUS       BC014995                3467 bp    mRNA    linear   PRI 12-SEP-2002
DEFINITION  Homo sapiens, clone IMAGE:4850025, mRNA.
ACCESSION   BC014995
VERSION     BC014995.1  GI:21955407
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3467)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-OCT-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
            Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
            Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
            Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
            Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
            Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
            Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
            George Yang, Scott Zuyderduyn, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 34 Row: a Column: 19.
FEATURES              Location/Qualifiers
     source           1. .3467
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4850025"
                      /tissue_type="Spleen"
                      /clone_lib="NIH_MGC_113"
                      /lab_host="DH10B-R"
                      /note="Vector: pOTB7"
ORIGIN
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Alignment Scores:
Pred. No.:              2.18e-107       Length:         3467
Score:                  119.00          Matches:        182
Percent Similarity:     98.91%          Conservative:   0
Best Local Similarity:  98.91%          Mismatches:     1
Query Match:            39.27%          Indels:         2
DB:                     9               Gaps:           0

US-10-047-021-86 (1-303) x BC014995 (1-3467)

Qy         84 ProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGln 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCAG 61

Qy        104 AlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAla 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCA 121

Qy        124 ValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPro 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCCT 181

Qy        144 ArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGly 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGGC 241

Qy        164 HisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGly 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 CACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGGA 301

Qy        184 ArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu*** 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 AGGCACACAGTGTCCGGGGGATCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG- 360

Qy        204 -ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgVa 223
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GACCTACATGTGTGTGGCCACCAACAGCGCAGGACACAGGGAGAGCCGCGCAGCCCGGGT 420

Qy        223 lSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleGl 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCA 480

Qy        243 nLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProAl 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGGC 540

Qy        263 aValTrpLeu 266
              |||||||||
Db        541 GGTGTGGCTC 550
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```
RESULT 12
AP003501/c
LOCUS       AP003501               186971 bp    DNA     linear   PRI 08-MAR-2002
DEFINITION  Homo sapiens genomic DNA, chromosome 11q, clone:RP11-664I21,
            complete sequence.
ACCESSION   AP003501
VERSION     AP003501.2  GI:19263048
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Homo sapiens genomic DNA
  JOURNAL   Published Only in Database (2001)
REFERENCE   2  (bases 1 to 186971)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-APR-2001) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:13603460.
FEATURES             Location/Qualifiers
     source          1. .186971
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="11"
                     /map="11q"
                     /clone="RP11-664I21"
ORIGIN

Alignment Scores:
Pred. No.:              2.66e-66        Length:         186971
Score:                  79.00           Matches:        109
Percent Similarity:     98.20%          Conservative:   0
Best Local Similarity:  98.20%          Mismatches:     1
Query Match:            26.07%          Indels:         2
DB:                     9               Gaps:           0

US-10-047-021-86 (1-303) x AP003501 (1-186971)

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      32342 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 32283

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
              |||||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db      32282 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 32224

Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      32223 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 32164

Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      32163 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 32104

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      32103 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 32044

Qy        123 aValSerArgGlyAlaArgLeuSerValAla 133
              |||||||||||||||||||||||||||||
Db      32043 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCT 32013
```

```
RESULT 13
AK074163
LOCUS       AK074163               4694 bp    mRNA    linear   PRI 15-FEB-2002
DEFINITION  Homo sapiens mRNA for FLJ00236 protein.
ACCESSION   AK074163
VERSION     AK074163.1  GI:18676673
KEYWORDS    fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
  TITLE     The nucleotide sequence of a long cDNA clone isolated from human
            spleen
  JOURNAL   Published Only in Database (2002)
REFERENCE   2  (bases 1 to 4694)
  AUTHORS   Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research
            Institute, Department of Human Gene Research; 1532-3, Yana,
            Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
            URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913,
            Fax:81-438-52-3914)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
```

Economy, Trade and Industry of Japan; cDNA full insert and 5'- & 3'-end one pass sequencing: Research Association for Biotechnology; cDNA library construction and clone selection: Kazusa DNA Research Institute.

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FEATURES             Location/Qualifiers
     source          1. .4694
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="FLJ00236"
                     /tissue_type="spleen"
                     /dev_stage="adult"
                     /note="vector:pBluescriptII SK plus"
     gene            1. .4694
                     /gene="FLJ00236"
     CDS             <1. .2109
                     /gene="FLJ00236"
                     /note="Start codon is not identified."
                     /codon_start=1
                     /evidence=not_experimental
                     /product="FLJ00236 protein"
                     /protein_id="BAB84989.1"
                     /db_xref="GI:18676674"
                     /translation="MGSGGDSLLGGRGSLPLLLLLIMVLREDFQIQPRDMVAVVGEQF
                     TLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTYMCVATNS
                     AGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLSWKV
                     SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSG
                     RARGPDSNVLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWS
                     LGNTSLPPANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAME
                     RATQEPSEHGPWTLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPG
                     LYRYTSEDAILKHRMDHSDSQWLADTWRSTGSGRDLSSSSSLSSRLGADARDPLDCRR
                     SLLSWDSRSPGVPLLPDTSTFYGSLIAELPSSTPARPSPQVPAVRRLPPQLAQLSSPC
                     SSSDSLCSRRGLSSPRLSLAPAEAWKAKKKQELQHANSSPLLRDSHSLELRACELGNR
                     GSKNLSQSPGAVPQALVAWRALGPKLLSSSNELVTRHLPPAPLFPHETPPTQSQQTQP
                     PVAPQAPSSILLPAAPIPILSPCSPPSPQASSLSGPSPASSRLSSSSLSSLGEDQDSV
                     LTPEEVALCLELSEGEETPR"
ORIGIN
```

Alignment Scores:

Pred. No.:	9.4e-58	Length:	4694
Score:	69.00	Matches:	132
Percent Similarity:	98.51%	Conservative:	0
Best Local Similarity:	98.51%	Mismatches:	1
Query Match:	22.77%	Indels:	2
DB:	9	Gaps:	0

US-10-047-021-86 (1-303) x AK074163 (1-4694)

```
Qy        134 ValLeuArgGluAspPheGlnIleGlnProArgAspMetValAlaValValGlyGluGln 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 GTCCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAG 129

Qy        154 PheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTrpLys 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 TTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAA 189

Qy        174 AspGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSerGlyGlySerLeuLeu 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GATGGGAAACCCCTGGCCCTCCAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTG 249

Qy        194 MetAlaArgAlaGluLysSerAspGlu***-ThrTyrMetCysValAlaThrAsnSerAl 213
              |||||||||||||||||||||||||||    |||||||||||||||||||||||||||||
Db        250 ATGGCAAGAGCAGAGAAGAGTGACGAAGG-GACCTACATGTGTGTGGCCACCAACAGCGC 308

Qy        213 aGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGl 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 AGGACATAGGGAGAGCCGCGCAGCCCGGGTTTCCATCCAGGAGCCCCAGGACTACACGGA 368

Qy        233 uProValGluLeuLeuAlaValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAs 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GCCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAAATGTGACACTGCTGAACCCGGA 428

Qy        253 pProAlaGluGlyProLysProArgProAlaValTrpLeu 266
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              ||||||||||||||||||||||||||||||||||||||||
Db        429 TCCTGCAGAGGGCCCCAAGCCTAGACCGGCGGTGTGGCTC 468
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```
RESULT 14
BD204437
LOCUS       BD204437                232 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  5'EST and human protein encoded thereby.
ACCESSION   BD204437
VERSION     BD204437.1  GI:33014207
KEYWORDS    JP 2002511259-A/641.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 232)
  AUTHORS   Edwards,J.B.D.M., Duclert,A. and Giordano,J.Y.
  TITLE     5'EST and human protein encoded thereby
  JOURNAL   Patent: JP 2002511259-A 641 16-APR-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002511259-A/641
            PD   16-APR-2002
            PF   09-APR-1999 JP 2000543599
            PR   09-APR-1998 US    09/057719,28-APR-1998 US    09/069047 PI
            JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,JEAN YVES  PI
            GIORDANO
            PC   C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12M1/00,C12N1/15, PC
             C12N1/19,
            PC   C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/53,G01N33/566, PC
             G06F17/50//
            PC   G06F17/30,C12N15/00,C12N5/00,C12N15/00
            CC   Von Heijne matrix
            CC   score 3.79999995231628
            CC   seq LPLLLPAHHGRHG/SG
            FH   Key             Location/Qualifiers
            FT   CDS             41. .232
            FT   sig_peptide     41. .121.
FEATURES             Location/Qualifiers
     source          1. .232
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN
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Alignment Scores:

Pred. No.:	3.88e-30	Length:	232
Score:	40.00	Matches:	53
Percent Similarity:	98.15%	Conservative:	0
Best Local Similarity:	98.15%	Mismatches:	0
Query Match:	13.20%	Indels:	1
DB:	6	Gaps:	0

US-10-047-021-86 (1-303) x BD204437 (1-232)

```
Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeu-Le 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db         41 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCCT 100

Qy         20 uLeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAs 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 GCTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGA 160

Qy         40 pGlnLeuPheGlnGlyProGlyProAlaArgMetSerCys 53
              |||||||||||||||||||||||||||||||||||||||||
Db        161 CCAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGC 200
```

```
RESULT 15
AY277635
LOCUS       AY277635                2886 bp    mRNA    linear   ROD 12-MAY-2003
DEFINITION  Rattus norvegicus ROBO4 (Robo4) mRNA, complete cds.
ACCESSION   AY277635
VERSION     AY277635.1  GI:30575794
KEYWORDS    .
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```
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 2886)
  AUTHORS   Roberts,K.G. and Stewart,L.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-2003) CRT Development Laboratory, Cancer Research
            Technology, Suite 23, Dominion House, 59 Bartholomew Close, London,
            England EC1A 7BE, United Kingdom
FEATURES             Location/Qualifiers
     source          1. .2886
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
     gene            1. .2886
                     /gene="Robo4"
     CDS             1. .2886
                     /gene="Robo4"
                     /note="ROBO4-I; similar to Homo sapiens and Mus musculus
                     ROBO4"
                     /codon_start=1
                     /product="ROBO4"
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DB:                     10              Gaps:           0

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Job time : 4490 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 29, 2004, 08:17:17 ; Search time 52 Seconds
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Title: US-10-047-021-86
Perfect score: 303
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Gapop 60.0 , Gapext 60.0

Searched: 809742 seqs, 211153259 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	300	99.0	303	15	US-10-047-021-86	Sequence 86, Appl
2	300	99.0	304	14	US-10-411-224-86	Sequence 86, Appl
3	148	48.8	480	10	US-09-796-753-158	Sequence 158, App
4	148	48.8	985	9	US-09-978-295A-211	Sequence 211, App
5	148	48.8	985	9	US-09-978-697-211	Sequence 211, App
6	148	48.8	985	9	US-09-978-192A-211	Sequence 211, App
7	148	48.8	985	9	US-09-999-832A-211	Sequence 211, App
8	148	48.8	985	10	US-09-978-189-211	Sequence 211, App
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45	148	48.8	985	14	US-10-017-191A-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-10-047-021-86
; Sequence 86, Application US/10047021
; Publication No. US20040002591A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: PZ016P2
; CURRENT APPLICATION NUMBER: US/10/047,021
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/262,066
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 09/722,329
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/262,109
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: PCT/US98/18360
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: US 60/057,626
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/057,663
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/057,669
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/058,667
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/058,974
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/058,973
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/058,666
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: US 60/090,112
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 303

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;   ORGANISM: Homo sapiens
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;   NAME/KEY: SITE
;   LOCATION: (203)
;   OTHER INFORMATION: Xaa equals any amino acid
;   NAME/KEY: SITE
;   LOCATION: (267)
;   OTHER INFORMATION: Xaa equals any amino acid
;   NAME/KEY: SITE
;   LOCATION: (274)
;   OTHER INFORMATION: Xaa equals any amino acid
US-10-047-021-86

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  Best Local Similarity   100.0%;  Pred. No. 3.9e-262;
  Matches  303;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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US-10-411-224-86
; Sequence 86, Application US/10411224
; Publication No. US20030166906A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 50 Human Secreted Proteins
;  FILE REFERENCE: PZ016P1
;  CURRENT APPLICATION NUMBER: US/10/411,224
;  CURRENT FILING DATE:  2003-04-11
;  PRIOR APPLICATION NUMBER: US/09/722,329
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: 09/262,109
;  PRIOR FILING DATE: 1999-03-04
;  PRIOR APPLICATION NUMBER: 60/057,626
;  PRIOR FILING DATE: 1997-09-05
;  PRIOR APPLICATION NUMBER: 60/057,663
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;  PRIOR APPLICATION NUMBER: 60/058,973
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/058,666
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 206
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
;   LENGTH: 304
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (203)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (267)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (274)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (304)
;   OTHER INFORMATION: Xaa equals stop translation
US-10-411-224-86

  Query Match             99.0%;  Score 300;  DB 14;  Length 304;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-262;
  Matches  303;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        301 NTG 303
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RESULT 3
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; Publication No. US20030027998A1
; GENERAL INFORMATION:
;  APPLICANT:  McCarthy, Sean A.
;  TITLE OF INVENTION:  SECRETED PROTEINS AND USES THEREOF
;  FILE REFERENCE:  7853-227-999
;  CURRENT APPLICATION NUMBER: US/09/796,753
;  CURRENT FILING DATE:  2001-03-01
;  PRIOR APPLICATION NUMBER:  09/183,175
;  PRIOR FILING DATE:  1998-10-30
;  PRIOR APPLICATION NUMBER:  09/223,094
;  PRIOR FILING DATE:  1998-12-30
;  PRIOR APPLICATION NUMBER:  09/223,546
;  PRIOR FILING DATE:  1998-12-30
;  PRIOR APPLICATION NUMBER:  09/224,246
;  PRIOR FILING DATE:  1998-12-30
;  PRIOR APPLICATION NUMBER:  09/259,388
;  PRIOR FILING DATE:  1999-02-26
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; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 158
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-158

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Best Local Similarity 100.0%; Pred. No. 6.1e-125;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-978-295A-211
; Sequence 211, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 48.8%; Score 148; DB 9; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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; Sequence 211, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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RESULT 6
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; Sequence 211, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:

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; APPLICANT: Botstein, David
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.8%; Score 148; DB 9; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
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Db         33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy        115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
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Db         93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy        175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
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Db        153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
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RESULT 7
US-09-999-832A-211
; Sequence 211, Application US/09999832A
; Publication No. US20020192706A1

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.8%; Score 148; DB 9; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
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Db         33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

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Db         93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy        175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
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Db        153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
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RESULT 8
US-09-978-189-211
; Sequence 211, Application US/09978189

; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.8%; Score 148; DB 10; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
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Db         33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy        115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
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Db         93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy        175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
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Db        153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
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RESULT 9
US-09-978-608A-211

; Sequence 211, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 211
; LENGTH: 985
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-211

Query Match 48.8%; Score 148; DB 10; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
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Db         33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy        115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy        175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
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Db        153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
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RESULT 10
US-09-978-585A-211
; Sequence 211, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 211
; LENGTH: 985
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-211

Query Match 48.8%; Score 148; DB 10; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy        115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy        175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
              ||||||||||||||||||||||||||||
Db        153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
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RESULT 11
US-09-978-191A-211
; Sequence 211, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
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; PRIOR APPLICATION NUMBER: 60/077641
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; PRIOR APPLICATION NUMBER: 60/077649
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; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
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; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-04-22
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.8%; Score 148; DB 10; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy         115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy         175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
               ||||||||||||||||||||||||||||
Db         153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
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RESULT 12
US-09-978-403A-211
; Sequence 211, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/085339
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; PRIOR APPLICATION NUMBER: 60/085338
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; PRIOR APPLICATION NUMBER: 60/085323
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
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; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.8%; Score 148; DB 10; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy        115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy        175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
              ||||||||||||||||||||||||||||
Db        153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
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RESULT 13
US-09-978-564A-211
; Sequence 211, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.8%; Score 148; DB 10; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
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Db         153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
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RESULT 14
US-09-999-833A-211
; Sequence 211, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 48.8%; Score 148; DB 10; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
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RESULT 15
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; Sequence 211, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.

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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441

; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 48.8%; Score 148; DB 10; Length 985;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
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Db          33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy         115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy         175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
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Db         153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
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Search completed: February 29, 2004, 08:23:55
Job time : 56 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 29, 2004, 08:16:48 ; Search time 23 Seconds
(without alignments)
680.116 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 303
Sequence: 1 MGSGGDSLLGGRGSLPLLLL.....SGPRLPREARELRGQRRNTG 303

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10	3.3	1209	4	US-09-130-158A-2	Sequence 2, Appli
2	8	2.6	118	4	US-09-621-976-4124	Sequence 4124, Ap
3	8	2.6	161	4	US-09-673-395A-577	Sequence 577, App
4	8	2.6	189	2	US-08-837-029-2	Sequence 2, Appli
5	8	2.6	287	4	US-09-800-729-114	Sequence 114, App
6	8	2.6	287	4	US-09-800-729-153	Sequence 153, App
7	8	2.6	330	4	US-09-615-192A-284	Sequence 284, App
8	8	2.6	613	4	US-09-800-729-82	Sequence 82, Appl
9	8	2.6	613	4	US-09-800-729-98	Sequence 98, Appl
10	8	2.6	1501	2	US-08-447-464-3	Sequence 3, Appli
11	8	2.6	1501	2	US-08-716-679-3	Sequence 3, Appli
12	8	2.6	1911	1	US-08-348-006B-5	Sequence 5, Appli
13	8	2.6	1911	2	US-08-800-825A-5	Sequence 5, Appli
14	8	2.6	1911	3	US-09-158-657-5	Sequence 5, Appli
15	8	2.6	1911	5	PCT-US94-10166-5	Sequence 5, Appli
16	7	2.3	15	5	PCT-US93-06751-29	Sequence 29, Appl
17	7	2.3	57	2	US-08-318-837-50	Sequence 50, Appl
18	7	2.3	66	4	US-09-540-236-2630	Sequence 2630, Ap
19	7	2.3	77	3	US-09-246-500B-14	Sequence 14, Appl
20	7	2.3	77	4	US-09-621-976-4010	Sequence 4010, Ap
21	7	2.3	94	4	US-09-858-664A-23	Sequence 23, Appl
22	7	2.3	94	4	US-10-274-978-24	Sequence 24, Appl
23	7	2.3	119	4	US-09-858-664A-30	Sequence 30, Appl
24	7	2.3	119	4	US-10-274-978-31	Sequence 31, Appl
25	7	2.3	126	1	US-08-276-852-142	Sequence 142, App
26	7	2.3	126	1	US-08-899-575-142	Sequence 142, App
27	7	2.3	126	1	US-08-899-575-142	Sequence 142, App
28	7	2.3	126	5	PCT-US95-08743-142	Sequence 142, App
29	7	2.3	134	4	US-09-621-976-3902	Sequence 3902, Ap
30	7	2.3	155	4	US-09-543-681A-4921	Sequence 4921, Ap
31	7	2.3	158	4	US-09-252-991A-32569	Sequence 32569, A
32	7	2.3	185	4	US-09-252-991A-26514	Sequence 26514, A
33	7	2.3	187	4	US-09-252-991A-29971	Sequence 29971, A
34	7	2.3	204	4	US-09-252-991A-30186	Sequence 30186, A
35	7	2.3	209	1	US-08-455-001-2	Sequence 2, Appli
36	7	2.3	209	3	US-08-308-814-2	Sequence 2, Appli
37	7	2.3	209	4	US-09-214-631-6	Sequence 6, Appli
38	7	2.3	209	5	PCT-US95-11869-2	Sequence 2, Appli
39	7	2.3	213	1	US-09-609-324A-10	Sequence 10, Appl
40	7	2.3	213	2	US-08-920-440B-10	Sequence 10, Appl
41	7	2.3	213	3	US-09-173-492-10	Sequence 10, Appl
42	7	2.3	213	3	US-09-173-133-10	Sequence 10, Appl
43	7	2.3	213	4	US-09-580-236A-10	Sequence 10, Appl
44	7	2.3	223	4	US-10-162-012-9	Sequence 9, Appli
45	7	2.3	230	3	US-08-952-235-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-130-158A-2
; Sequence 2, Application US/09130158A
; Patent No. 6576607
; GENERAL INFORMATION:
; APPLICANT: Schachner, Melitta
; TITLE OF INVENTION: CNS Neurite Outgrowth Modulators and
; TITLE OF INVENTION: Compositions, Cells and Method Embodying and Using Same
; FILE REFERENCE: 1094-1-001 CIP1B
; CURRENT APPLICATION NUMBER: US/09/130,158A
; CURRENT FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: US 08/636,514
; PRIOR FILING DATE: 1996-04-19
; PRIOR APPLICATION NUMBER: US 08/483,959
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/424,995
; PRIOR FILING DATE: 1995-04-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1209
; TYPE: PRT
; ORGANISM: murine
US-09-130-158A-2

Query Match 3.3%; Score 10; DB 4; Length 1209;
Best Local Similarity 100.0%; Pred. No. 0.77;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        116 ASNRLGTAVS 125
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Db        111 ASNRLGTAVS 120
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RESULT 2
US-09-621-976-4124
; Sequence 4124, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4124
; LENGTH: 118

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20..-1
; NAME/KEY: UNSURE
; LOCATION: -16
; OTHER INFORMATION: Xaa = Ala,Gly
US-09-621-976-4124

  Query Match 2.6%; Score 8; DB 4; Length 118;
  Best Local Similarity 100.0%; Pred. No. 6.8;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 SLPLLLLL 21
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Db 98 SLPLLLLL 105

RESULT 3
US-09-673-395A-577
; Sequence 577, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 577
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (15)
; OTHER INFORMATION: Any, other, or unknown amino acid
; NAME/KEY: MOD_RES
; LOCATION: (20)..(21)
; OTHER INFORMATION: Any, other, or unknown amino acid
; NAME/KEY: MOD_RES
; LOCATION: (35)
; OTHER INFORMATION: Any, other, or unknown amino acid
; NAME/KEY: MOD_RES
; LOCATION: (39)
; OTHER INFORMATION: Any, other, or unknown amino acid
; NAME/KEY: MOD_RES
; LOCATION: (45)
; OTHER INFORMATION: Any, other, or unknown amino acid
; NAME/KEY: MOD_RES
; LOCATION: (80)
; OTHER INFORMATION: Any, other, or unknown amino acid
; NAME/KEY: MOD_RES
; LOCATION: (85)
; OTHER INFORMATION: Any, other, or unknown amino acid
; NAME/KEY: MOD_RES
; LOCATION: (87)
; OTHER INFORMATION: Any, other, or unknown amino acid
US-09-673-395A-577

  Query Match 2.6%; Score 8; DB 4; Length 161;
  Best Local Similarity 100.0%; Pred. No. 9.1;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LPLLLLLI 22
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Db 2 LPLLLLLI 9

RESULT 4
US-08-837-029-2
; Sequence 2, Application US/08837029
; Patent No. 5945303
; GENERAL INFORMATION:
; APPLICANT: Wei et al.
; TITLE OF INVENTION: Human Hematopoietic - Specific Protein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,029
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/04930
; FILING DATE: 11-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-837-029-2

  Query Match 2.6%; Score 8; DB 2; Length 189;
  Best Local Similarity 100.0%; Pred. No. 11;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 SLPLLLLL 21
       ||||||||
Db 4 SLPLLLLL 11

RESULT 5
US-09-800-729-114
; Sequence 114, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
; LENGTH: 287
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-800-729-114

Query Match 2.6%; Score 8; DB 4; Length 287;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 SLPLLLLL 21
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Db 12 SLPLLLLL 19

RESULT 6
US-09-800-729-153
; Sequence 153, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 153
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-153

Query Match 2.6%; Score 8; DB 4; Length 287;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 SLPLLLLL 21
||||||||
Db 12 SLPLLLLL 19

RESULT 7
US-09-615-192A-284
; Sequence 284, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003c4U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 284
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-615-192A-284

Query Match 2.6%; Score 8; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 SLPLLLLL 21
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Db 18 SLPLLLLL 25

RESULT 8
US-09-800-729-82
; Sequence 82, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-82

Query Match 2.6%; Score 8; DB 4; Length 613;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 SLPLLLLL 21
||||||||
Db 12 SLPLLLLL 19

RESULT 9
US-09-800-729-98
; Sequence 98, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (507)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-800-729-98

Query Match 2.6%; Score 8; DB 4; Length 613;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 SLPLLLLL 21
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Db 12 SLPLLLLL 19

RESULT 10
US-08-447-464-3

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; Sequence 3, Application US/08447464
; Patent No. 5840842
;  GENERAL INFORMATION:
;    APPLICANT:  Schlessinger, Joseph
;    APPLICANT:  Yan, Hai
;    TITLE OF INVENTION:  NOVEL RECEPTOR-TYPE PROTEIN
;    TITLE OF INVENTION:  PHOSPHOTYROSINE PHOSPHATASE-SIGMA
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/447,464
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/130,570
;      FILING DATE:  01-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7683-043
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-8864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1501 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-447-464-3

  Query Match             2.6%;  Score 8;  DB 2;  Length 1501;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        207 CVATNSAG 214
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Db        207 CVATNSAG 214


RESULT 11
US-08-716-679-3
; Sequence 3, Application US/08716679
; Patent No. 5846800
;  GENERAL INFORMATION:
;    APPLICANT:  Schlessinger, Joseph
;    APPLICANT:  Yan, Hai
;    TITLE OF INVENTION:  NOVEL RECEPTOR-TYPE PROTEIN
;    TITLE OF INVENTION:  PHOSPHOTYROSINE PHOSPHATASE-SIGMA
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/716,679
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/130,570
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  7683-043
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-8864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1501 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-716-679-3

  Query Match             2.6%;  Score 8;  DB 2;  Length 1501;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        207 CVATNSAG 214
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Db        207 CVATNSAG 214


RESULT 12
US-08-348-006B-5
; Sequence 5, Application US/08348006B
; Patent No. 5658756
;  GENERAL INFORMATION:
;    APPLICANT:  RODAN, GIDEON A.
;    APPLICANT:  SCHMIDT, AZRIEL
;    APPLICANT:  RUTLEDGE, SU JANE
;    TITLE OF INVENTION:  CDNA ENCODING A NOVEL HUMAN PROTEIN
;    TITLE OF INVENTION:  TYROSINE PHOSPHATASE
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND
;      STREET:  126 E. LINCOLN AVE., P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/348,006B
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/122,032
;      FILING DATE:  14-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, J., MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  18992IA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-3905
;      TELEFAX:  908-594-4720
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1911 amino acids
```

```
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-348-006B-5

  Query Match             2.6%;  Score 8;  DB 1;  Length 1911;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        207 CVATNSAG 214
              ||||||||
Db        207 CVATNSAG 214


RESULT 13
US-08-800-825A-5
; Sequence 5, Application US/08800825A
; Patent No. 5866397
;  GENERAL INFORMATION:
;    APPLICANT:  RODAN, GIDEON A.
;    APPLICANT:  SCHMIDT, AZRIEL
;    APPLICANT:  RUTLEDGE, SU JANE
;    TITLE OF INVENTION:  CDNA ENCODING A NOVEL HUMAN PROTEIN
;    TITLE OF INVENTION:  TYROSINE PHOSPHATASE
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 E. LINCOLN AVE., P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/800,825A
;      FILING DATE:  14-FEB-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, J. MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  18992DA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  732-594-3905
;      TELEFAX:  732-594-4720
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1911 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-800-825A-5

  Query Match             2.6%;  Score 8;  DB 2;  Length 1911;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        207 CVATNSAG 214
              ||||||||
Db        207 CVATNSAG 214


RESULT 14
US-09-158-657-5
; Sequence 5, Application US/09158657
; Patent No. 6214564
;  GENERAL INFORMATION:
;    APPLICANT:  RODAN, GIDEON A.
;    APPLICANT:  SCHMIDT, AZRIEL
;    APPLICANT:  RUTLEDGE, SU JANE
;    TITLE OF INVENTION:  CDNA ENCODING A NOVEL HUMAN PROTEIN
;    TITLE OF INVENTION:  TYROSINE PHOSPHATASE
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  J. MARK HAND - MERCK & CO., INC.
;      STREET:  126 E. LINCOLN AVE., P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07065-0900
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/158,657
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/800,825
;      FILING DATE:  14-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAND, J. MARK
;      REGISTRATION NUMBER:  36,545
;      REFERENCE/DOCKET NUMBER:  18992DA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  732-594-3905
;      TELEFAX:  732-594-4720
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1911 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-158-657-5

  Query Match             2.6%;  Score 8;  DB 3;  Length 1911;
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  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        207 CVATNSAG 214
              ||||||||
Db        207 CVATNSAG 214


RESULT 15
PCT-US94-10166-5
; Sequence 5, Application PC/TUS9410166
;  GENERAL INFORMATION:
;    APPLICANT:  RODAN, GIDEON A
;    APPLICANT:  SCHMIDT, AZRIEL
;    APPLICANT:  RUTLEDGE, SU JANE
;    TITLE OF INVENTION:  CDNA ENCODING A NOVEL HUMAN PROTEIN
;    TITLE OF INVENTION:  TYROSINE PHOSPHATASE
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JOHN W. WALLEN III
;      STREET:  P.O. BOX 2000, 126 E. LINCOLN AVE.
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10166
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;       FILING DATE:  09-SEPT-1994
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/122,032
;       FILING DATE:  14-SEP-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WALLEN, JOHN W III
;       REGISTRATION NUMBER:  35403
;       REFERENCE/DOCKET NUMBER:  18992
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  908-594-3905
;       TELEFAX:  908-594-4720
;       TELEX:  138825
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1911 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US94-10166-5

  Query Match             2.6%;  Score 8;  DB 5;  Length 1911;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        207 CVATNSAG 214
              ||||||||
Db        207 CVATNSAG 214


Search completed: February 29, 2004, 08:19:35
Job time : 25 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 27, 2004, 15:39:59 ; Search time 76 Seconds
(without alignments)
1126.472 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 303
Sequence: 1 MGSGGDSLLGGRGSLPLLLL.....SGPRLPREARELRGQRRNTG 303

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	300	99.0	303	5	ABP62033	Abp62033 Human sec
2	300	99.0	304	2	AAY12934	Aay12934 Amino aci
3	148	48.8	480	4	AAU00501	Aau00501 Human TAN
4	148	48.8	985	2	AAY41716	Aay41716 Human PRO
5	148	48.8	985	3	AAB44272	Aab44272 Human PRO
6	148	48.8	985	6	ABO25218	Abo25218 Novel hum
7	148	48.8	985	6	ABU72224	Abu72224 Novel hum
8	148	48.8	985	6	ABU84904	Abu84904 Human sec
9	148	48.8	985	6	ABU61102	Abu61102 Human PRO
10	148	48.8	985	6	ABU80371	Abu80371 Human sec
11	148	48.8	985	6	ADA24750	Ada24750 Novel hum
12	148	48.8	985	6	ABO19673	Abo19673 Novel hum
13	148	48.8	985	6	ADA12411	Ada12411 Human sec
14	148	48.8	985	6	ABO19564	Abo19564 Novel hum
15	148	48.8	985	7	ADB73717	Adb73717 Human PRO
16	148	48.8	985	7	ADB76433	Adb76433 Human PRO
17	148	48.8	985	7	ADC43859	Adc43859 Human sec
18	148	48.8	985	7	ADC61619	Adc61619 Human sec
19	148	48.8	985	7	ADC63583	Adc63583 Human sec
20	148	48.8	985	7	ADC66683	Adc66683 Human sec
21	148	48.8	985	7	ADC68807	Adc68807 Human sec
22	148	48.8	985	7	ADC62867	Adc62867 Human sec
23	148	48.8	985	7	ADC67932	Adc67932 Human sec
24	148	48.8	985	7	ADC41252	Adc41252 Human sec
25	148	48.8	985	7	ADC67307	Adc67307 Human sec
26	148	48.8	985	7	ADC62243	Adc62243 Human sec
27	148	48.8	985	7	ADC41876	Adc41876 Human sec
28	148	48.8	985	7	ADE49245	Ade49245 Human sec
29	148	48.8	985	7	ADE35299	Ade35299 Human sec
30	148	48.8	985	7	ADE16413	Ade16413 Human sec
31	148	48.8	985	7	ADD73028	Add73028 Human sec
32	148	48.8	985	7	ADD72386	Add72386 Human sec
33	148	48.8	985	7	ADE17037	Ade17037 Human sec
34	148	48.8	985	8	ADE48545	Ade48545 Human sec
35	148	48.8	985	8	ADE89646	Ade89646 Human sec
36	148	48.8	1007	5	ABB97310	Abb97310 Novel hum
37	148	48.8	1104	5	AAU99419	Aau99419 Human ECS
38	120	39.6	792	4	AAB95515	Aab95515 Human pro
39	120	39.6	792	4	AAG67430	Aag67430 Amino aci
40	110	36.3	934	4	AAU00500	Aau00500 Human TAN
41	27	8.9	1015	5	AAU99420	Aau99420 Mouse ECS
42	20	6.6	20	5	AAU99411	Aau99411 Human ECS
43	19	6.3	64	3	AAY65275	Aay65275 Human 5'
44	12	4.0	12	5	AAU99410	Aau99410 Human ECS
45	10	3.3	10	5	AAU99412	Aau99412 Human ECS

ALIGNMENTS

RESULT 1
ABP62033
ID ABP62033 standard; protein; 303 AA.
XX
AC ABP62033;
XX
DT 12-NOV-2002 (first entry)
XX
DE Human secreted protein SEQ ID NO 86.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO200257420-A2.
XX
PD 25-JUL-2002.
XX
PF 17-JAN-2002; 2002WO-US001109.
XX
PR 18-JAN-2001; 2001US-0262066P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA, Ruben SM, Lafleur DW, Shi Y, Rosen CA, Olsen H;
PI Ebner R, Brewer LA;
XX
DR WPI; 2002-599716/64.
DR N-PSDB; ABQ92573.
XX
PT New polynucleotides and polypeptides useful for diagnosing, prognosing,
PT treating or preventing e.g. neurodegenerative, central nervous system,
PT autoimmune, respiratory, reproductive, or inflammatory diseases or
PT disorders.
XX
PS Claim 11; Fig 1; 785pp; English.
XX
CC The invention relates to novel genes (ABQ92553-ABQ92607) and proteins
CC (ABP62013-ABP62153) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in

```
CC   the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC   ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC   breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC   disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC   anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC   multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC   cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC   ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC   infectious diseases such as viral, bacterial, fungal and parasitic
CC   infections
XX
SQ   Sequence 303 AA;

  Query Match             99.0%;  Score 300;  DB 5;  Length 303;
  Best Local Similarity   100.0%;  Pred. No. 1e-273;
  Matches  303;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGSGGDSLLGGRGSLPLLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGSGGDSLLGGRGSLPLLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPP 60

Qy         61 PTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRL 120

Qy        121 GTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL 180

Qy        181 QPGRHTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
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Qy        241 RIQLENVTLLNPDPAEGPKPRPAVWLXWKVSGPXRLPNLTRPCSGPRLPREARELRGQRR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RIQLENVTLLNPDPAEGPKPRPAVWLXWKVSGPXRLPNLTRPCSGPRLPREARELRGQRR 300

Qy        301 NTG 303
              |||
Db        301 NTG 303


RESULT 2
AAY12934
ID   AAY12934 standard; protein; 304 AA.
XX
AC   AAY12934;
XX
DT   17-JUN-1999  (first entry)
XX
DE   Amino acid sequence of a human secreted peptide.
XX
KW   Human secreted protein; cancer; immune disorder; infection;
KW   inflammatory disorder; skin disorder; tumour; atherosclerosis;
KW   restenosis; autoimmune disorder; Alzheimer's disease;
KW   peripheral neuropathy; trauma; spinal cord injury; allergy;
KW   hematopoietic disorder; skeletal disorder; neurological disorder;
KW   arthritic disorder; asthma; immunodeficiency disease; AIDS;
KW   transplant rejection; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .27
FT                   /note= "signal peptide"
FT   Protein         28. .303
FT                   /note= "secreted protein"
XX
PN   WO9911293-A1.
XX
PD   11-MAR-1999.
XX
PF   03-SEP-1998;   98WO-US018360.
XX
PR   05-SEP-1997;   97US-0057626P.
PR   05-SEP-1997;   97US-0057663P.
PR   05-SEP-1997;   97US-0057669P.
PR   12-SEP-1997;   97US-0058666P.
PR   12-SEP-1997;   97US-0058667P.
PR   12-SEP-1997;   97US-0058973P.
PR   12-SEP-1997;   97US-0058974P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Moore PA,  Ruben SM,  Lafleur DW,  Shi Y,  Rosen GA,  Olsen HS;
PI   Ebner R,  Brewer LA;
XX
DR   WPI; 1999-204988/17.
DR   N-PSDB; AAX51721.
XX
PT   New isolated human genes and the secreted polypeptides they encode -
PT   useful for diagnosis and treatment of e.g. neurological disorders,
PT   tumors, immune disorders, inflammation or hematological disorders.
XX
PS   Claim 11; Page 190-191; 215pp; English.
XX
CC   AAY12914-68 represent human secreted proteins. The polypeptides and their
CC   corresponding polynucleotides are useful for preventing, treating or
CC   ameliorating medical conditions, e.g. by protein or gene therapy.
CC   Pathological conditions can also be diagnosed by determining the amount
CC   of the new polypeptides in a sample or by determining the presence of
CC   mutations in the new polynucleotides. Specific uses are described for
CC   each polynucleotide, based on which tissues they are most highly
CC   expressed in, and include developing products for the diagnosis or
CC   treatment of cancer, immune disorders, infection, inflammatory disorders,
CC   skin disorders, tumours, atherosclerosis, restenosis, autoimmune
CC   disorders, Alzheimer's disease, peripheral neuropathies, trauma, spinal
CC   cord injuries, allergy, hematopoietic disorders, skeletal disorders,
CC   neurological disorders, arthritic disorders, asthma, immunodeficiency
CC   diseases, AIDS and transplant rejection. The polypeptides are also useful
CC   for identifying their binding partners
XX
SQ   Sequence 304 AA;

  Query Match             99.0%;  Score 300;  DB 2;  Length 304;
  Best Local Similarity   100.0%;  Pred. No. 1e-273;
  Matches  303;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGSGGDSLLGGRGSLPLLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGSGGDSLLGGRGSLPLLLLLIMGGMAQDSPPQILVHPQDQLFQGPGPARMSCRASGQPP 60

Qy         61 PTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRL 120

Qy        121 GTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL 180
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Db        121 GTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLAL 180

Qy        181 QPGRHTVSGGSLLMARAEKSDEXTYMCVATNSAGHRESRAARVSIQEPQDYTEPVELLAV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 RIQLENVTLLNPDPAEGPKPRPAVWLXWKVSGPXRLPNLTRPCSGPRLPREARELRGQRR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RIQLENVTLLNPDPAEGPKPRPAVWLXWKVSGPXRLPNLTRPCSGPRLPREARELRGQRR 300

Qy        301 NTG 303
              |||
Db        301 NTG 303


RESULT 3
AAU00501
ID   AAU00501 standard; protein; 480 AA.
```

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XX
AC   AAU00501;
XX
DT   18-JUL-2001  (first entry)
XX
DE   Human TANGO 330 form 2 protein.
XX
KW   Human; TANGO 315; clone Jthxe18le12; TANGO 330; TANGO 437; TANGO 480;
KW   cellular process regulator; gene therapy; astrocyte; cancer; Roundabout;
KW   adrenal cortex; hypoadrenalism; hyperadrenalism; neoplasia;
KW   cell proliferative disorder; neurological disorder; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /label= Signal_peptide
FT   Modified-site   15. .17
FT                   /note= "Protein kinase C phosphorylation site"
FT   Domain          21. .480
FT                   /label= Extracellular_domain
FT   Protein         21. .480
FT                   /label= Mature_TANGO_330_form_2_protein
FT   Modified-site   30. .33
FT                   /note= "cAMP and cGMP dependent protein kinase
FT                   phosphorylation site"
FT   Modified-site   44. .47
FT                   /note= "Casein kinase II phosphorylation site"
FT   Domain          77. .147
FT                   /label= Ig-like_domain
FT   Modified-site   93. .95
FT                   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   100. .105
FT                   /note= "N-myristylation site"
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FT   Modified-site   141. .146
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FT   Modified-site   148. .150
FT                   /note= "Protein kinase C phosphorylation site"
FT   Modified-site   152. .157
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FT   Modified-site   158. .163
FT                   /note= "N-myristylation site"
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FT                   /label= Ig-like_domain
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FT                   /note= "Casein kinase II phosphorylation site"
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FT   Modified-site   343. .348
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FT   Modified-site   420. .423
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   427. .430
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   435. .438
FT                   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   456. .461
FT                   /note= "N-myristylation site"
XX
PN   WO200123523-A2.
XX
PD   05-APR-2001.
XX
PF   02-OCT-2000; 2000WO-US027202.
XX
PR   30-SEP-1999;   99US-00409634.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kirst S,  Wrighton N,  Fraser CC;
XX
DR   WPI; 2001-235372/24.
DR   N-PSDB; AAS01695.
XX
PT   Isolated secreted proteins and their encoding nucleic acids are used for
PT   diagnosis and treatment of e.g. bacterial and viral infections,
PT   autoimmune diseases and inflammatory disorders.
XX
PS   Claim 9; Fig 14; 261pp; English.
XX
CC   The present sequence representing human TANGO 330 form 2 is isolated from
CC   cDNA clone Jthxe18le12 from a human astrocyte cDNA library. TANGO 330 is
CC   1 of 4 novel human transmembrane proteins which also includes TANGO 315
CC   (AAU00498-AAU00499), TANGO 437 (AAU00502) and TANGO 480 (AAU00503). The
CC   nucleic acids encoding these proteins are useful as modulating agents in
CC   regulating a variety of cellular processes and can be used to express the
CC   proteins in a host cell in gene therapy applications. Antisense nucleic
CC   acid molecules and expression vectors containing the TANGO nucleic acids
CC   are also described. Diagnostic assays can be used to detect genetic
CC   alterations in the TANGO nucleic acids and to identify compounds that
CC   bind to or modulate activity of the TANGO proteins. Anti-TANGO antibodies
CC   are used diagnostically to monitor protein levels in tissue as a clinical
CC   testing procedure. TANGO 330 shows homology to human Roundabout. TANGO
CC   330 nucleic acids and proteins may be used to diagnose, treat and monitor
CC   disorders of the adrenal cortex e.g. hypoadrenalism, hyperadrenalism, and
CC   neoplasia. They can also be used to treat cell proliferative disorders
CC   (e.g. cancer), and neurological disorders e.g. Alzheimer's disease
XX
SQ   Sequence 480 AA;

  Query Match             48.8%;  Score 148;  DB 4;  Length 480;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-130;
  Matches  148;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
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Db         86 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 145

Qy        115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
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Db        146 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 205

Qy        175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
              ||||||||||||||||||||||||||||
Db        206 GKPLALQPGRHTVSGGSLLMARAEKSDE 233


RESULT 4
AAY41716
ID   AAY41716 standard; protein; 985 AA.
XX
AC   AAY41716;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Human PRO860 protein sequence.
XX
KW   Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
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KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US005028.
XX
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
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PR 20-MAR-1998; 98US-0078939P.
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PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
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PR 05-MAY-1998; 98US-0084366P.
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PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
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PR 18-MAY-1998; 98US-0086023P.
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PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.
DR N-PSDB; AAZ34069.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
PS Claim 12; Fig 77; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
CC AAY41774 represent polynucleotide and polypeptide sequence given in the
CC exemplification of the present invention
XX
SQ Sequence 985 AA;

Query Match 48.8%; Score 148; DB 2; Length 985;
Best Local Similarity 100.0%; Pred. No. 3.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
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Db          33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy         115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
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Db          93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy         175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
               ||||||||||||||||||||||||||||
Db         153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
```

RESULT 5
AAB44272
ID AAB44272 standard; protein; 985 AA.

XX
AC AAB44272;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO860 (UNQ421) protein sequence SEQ ID NO:211.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW expressed sequence tag; detection; cancer.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US004341.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 23-JUN-1999; 99US-0141037P.
PR 26-JUL-1999; 99US-0145698P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
DR N-PSDB; AAC78502.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX
PS Claim 12; Fig 77; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytostatic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX
SQ Sequence 985 AA;

Query Match 48.8%; Score 148; DB 3; Length 985;
Best Local Similarity 100.0%; Pred. No. 3.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy        115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
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Db         93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy        175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
              ||||||||||||||||||||||||||||
Db        153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
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RESULT 6
ABO25218
ID ABO25218 standard; protein; 985 AA.
XX
AC ABO25218;
XX
DT 09-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO860.
XX
KW Human; secreted and transmembrane protein; PRO; virucide; gene therapy;
KW cell death; growth induction cascade; blood coagulation cascade;
KW viral infection.
XX
OS Homo sapiens.
XX
PN US2003050239-A1.
XX
PD 13-MAR-2003.
XX
PF 15-OCT-2001; 2001US-00978191.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
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PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
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PR 15-APR-1998; 98US-0081817P.

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PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
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PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
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PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
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PR 07-MAY-1998; 98US-0084598P.
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PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-0109304P.
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PR 22-DEC-1998; 98US-00218517.
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PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
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PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
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PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

Query Match 48.8%; Score 148; DB 6; Length 985;
Best Local Similarity 100.0%; Pred. No. 3.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy        115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy        175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
              ||||||||||||||||||||||||||||
Db        153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
```

RESULT 7
ABU72224
ID ABU72224 standard; protein; 985 AA.
XX
AC ABU72224;
XX
DT 16-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO860.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; inflammatory disease; organ failure;
KW atherosclerosis; cardiac injury; infertility; birth defect;
KW premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
KW gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
KW tissue typing.
XX
OS Homo sapiens.
XX
PN US2002192706-A1.
XX
PD 19-DEC-2002.
XX
PF 24-OCT-2001; 2001US-00999832.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98WO-US024855.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-328860/31.
DR N-PSDB; ACA63637.
XX
PT New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
PS Claim 12; Fig 77; 453pp; English.
XX

CC The invention describes an isolated nucleic acid (I) comprising, or which
CC is at least 80 % sequence identity to, or the full-length coding sequence
CC of, any of 118 300-2100 nucleotide sequences, which encodes its
CC corresponding PRO polypeptide selected from 118 100-700 amino acid
CC sequences, all given in the specification. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS, cancer, or diabetic complications. The nucleic
CC acids are useful as hybridisation probes, in chromosome and gene mapping,
CC and in generating antisense RNA or DNA. The polypeptides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
CC in tissue typing. This is the amino acid sequence of a novel human
CC secreted and transmembrane PRO polypeptide
XX
SQ Sequence 985 AA;

Query Match 48.8%; Score 148; DB 6; Length 985;
Best Local Similarity 100.0%; Pred. No. 3.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy     115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy     175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
           ||||||||||||||||||||||||||||
Db     153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
```

RESULT 8
ABU84904
ID ABU84904 standard; protein; 985 AA.
XX
AC ABU84904;
XX
DT 12-AUG-2003 (first entry)
XX
DE Human secreted and transmembrane polypeptide PRO860.
XX
KW Human; thrombolytic agent; interferon; interleukin; cytokine;
KW erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;
KW apoptosis related condition; AIDS; amyotrophic lateral sclerosis;
KW inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;
KW gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;
KW hypertension; myocardial ischaemia; kidney disease; carcinogenesis;
KW glomerulonephritis; lung disease; pulmonary hypertension; preeclampsia;
KW bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;
KW inflammatory bowel disease; reproductive disorder; premature labour.
XX
OS Homo sapiens.
XX
PN US2002177553-A1.
XX
PD 28-NOV-2002.
XX
PF 15-OCT-2001; 2001US-00978192.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.

PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-328499/31.
DR N-PSDB; ACA71801.
XX
PT New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
PT modulators of receptor-ligand interactions.
XX
PS Claim 12; SEQ ID NO 211; 55pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
CC in PRO polypeptide detection methods. The PRO polypeptide is useful for
CC linking a bioactive molecule to a cell. The PRO polypeptide or an
CC antibody against it is useful for modulating a biological activity of a
CC cell. The PRO polypeptide is useful in industrial applications including
CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
CC polypeptide is also useful as a thrombolytic agent, interferon,
CC interleukin, erythropoietin, colony stimulating factor and other
CC cytokines. The PRO polypeptide is useful for treating disease such as
CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,
CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,
CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
CC Parkinson's disease; cardiovascular disease e.g. hypertension and
CC myocardial ischaemia; kidney disease e.g. renal failure and
CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory
CC bowel disease; reproductive disorders e.g. premature labour and
CC preeclampsia; carcinogenesis. The present sequence represents the amino
CC acid sequence of a PRO polypeptide of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification but
CC was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20020177553
XX
SQ Sequence 985 AA;

Query Match 48.8%; Score 148; DB 6; Length 985;
Best Local Similarity 100.0%; Pred. No. 3.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy         115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy         175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
               ||||||||||||||||||||||||||||
Db         153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
```

RESULT 9
ABU61102
ID ABU61102 standard; protein; 985 AA.
XX
AC ABU61102;
XX
DT 08-MAY-2003 (first entry)
XX
DE Human PRO860 polypeptide.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW cardiac insufficiency; nervous system disorder; kidney disorder;
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;
KW antiarthritic; anti-tumour; vulnerary; antianaemic; dermatological;
KW cardiant.
XX
OS Homo sapiens.
XX
PN US2002169284-A1.
XX
PD 14-NOV-2002.
XX
PF 16-OCT-2001; 2001US-00978697.
XX
PR 26-MAY-1981; 81US-00267213.
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99WO-US005190.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.

PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-288163/28.
DR N-PSDB; ABX92441.
XX
PT Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies.
XX
PS Claim 12; Fig 77; 459pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The bioactive molecule maybe a
CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.
CC The PRO polypeptides are useful for treating immune disorders, diabetes
CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system
CC disorders, kidney disorders, bone and cartilage disorders or arthritis,
CC tumours, and wound healing. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and gene
CC mapping, in the generation of antisense RNA and DNA, in the preparation
CC of PRO polypeptides, for generating transgenic animals or knockout
CC animals, for the genetic analysis of individuals with genetic disorders,
CC and in gene therapy. ABU61071-ABU61164 represent the human PRO
CC polypeptides of the invention. Note: The sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 985 AA;

Query Match 48.8%; Score 148; DB 6; Length 985;
Best Local Similarity 100.0%; Pred. No. 3.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
Db 33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy 115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
Db 93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy 175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
Db 153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180

RESULT 10
ABU80371
ID ABU80371 standard; protein; 985 AA.
XX
AC ABU80371;
XX
DT 24-JUN-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO860.
XX
KW Human; secreted protein; transmembrane protein; PRO; malignancy; cancer;
KW ovarian cancer; colorectal cancer; sarcoma; leukaemia; lymphoma;
KW inflammatory disease; necrosis; atherosclerosis; infertility;
KW premature aging; psoriasis; inflammatory disease; renal disease;
KW arthritis; immune-mediated alopecia; stroke; encephalitis; hepatitis;
KW multiple sclerosis; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003004102-A1.
XX
PD 02-JAN-2003.
XX
PF 15-OCT-2001; 2001US-00978189.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.

PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-341189/32.
DR N-PSDB; ACA66182.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO337 or
PT PRO1559), useful for treating or diagnosing e.g. cancers,
PT atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple
PT sclerosis in mammals.
XX
PS Claim 12; Fig 77; 460pp; English.
XX
CC The invention relates to a new isolated nucleic acid molecule comprises a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 94 PRO polypeptides whose sequences are fully defined in the
CC specification; or (b) any of 94 nucleotide sequences fully defined in the
CC specification; or the full length coding sequence of any these 94
CC nucleotide sequences. Also included are an isolated PRO polypeptide
CC scoring at least 80% positives when compared to any of the PRO
CC polypeptide sequences cited above (or an isolated PRO polypeptide having
CC at least 80% amino acid sequence identity to: (a) an amino acid sequence
CC encoded by the nucleotide deposited with ATCC numbers listed in the
CC specification; (b) the PRO polypeptide, lacking its associated signal
CC peptide; or (c) an extracellular domain of the PRO polypeptide, with or
CC lacking its associated signal peptide), a vector comprising the nucleic
CC acid molecule, a host cell comprising the vector (and producing a PRO
CC polypeptide), a chimaeric molecule comprising the PRO polypeptide fused
CC to a heterologous amino acid sequence and an anti-PRO antibody. The PRO
CC polypeptides or polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. These are particularly useful for
CC detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,
CC colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease,
CC necrosis, atherosclerosis, infertility, premature aging, psoriasis,
CC inflammatory disease, renal disease, arthritis, immune-mediated alopecia,
CC stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. The present sequence represents a PRO polypeptide
XX
SQ Sequence 985 AA;

Query Match 48.8%; Score 148; DB 6; Length 985;
Best Local Similarity 100.0%; Pred. No. 3.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy        115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
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Db         93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy        175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
              ||||||||||||||||||||||||||||
Db        153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
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RESULT 11
ADA24750
ID ADA24750 standard; protein; 985 AA.
XX
AC ADA24750;
XX
DT 20-NOV-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO860.
XX
KW Human; secreted and transmembrane protein; PRO; tissue typing;
KW chromosome identification; vaccine; cancer; retinal disorder;
KW sports-related joint disorder; osteoarthritis; rheumatoid arthritis;
KW wound healing; obesity; diabetes; hearing loss;
KW cardiac insufficiency disorder; kidney disorder; nervous system disorder;
KW haemoglobin associated disorder.
XX

OS Homo sapiens.
XX
PN US2003050241-A1.
XX
PD 13-MAR-2003.
XX
PF 16-OCT-2001; 2001US-00978564.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
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PR 11-MAR-1998; 98US-0077632P.
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PR 20-MAR-1998; 98US-0078939P.
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PR 26-MAR-1998; 98US-0079656P.
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PR 31-MAR-1998; 98US-0080165P.
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PR 28-APR-1998; 98US-0083322P.
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PR 28-MAY-1998; 98US-0087098P.
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PR 26-JUN-1998; 98US-0090863P.
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PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 16-JUN-1999; 99US-0139557P.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.

PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-521814/49.
DR N-PSDB; ADA24749.
XX
PT New isolated PRO polypeptides for example extracellular, secreted and
PT membrane bound proteins, useful for modulating the biological activities
PT of cells and for treating, for example diabetes, cancer, rheumatoid
PT arthritis, and hearing loss.
XX
PS Claim 12; Fig 77; 461pp; English.
XX
CC The invention describes an isolated secreted and transmembrane (PRO)
CC polypeptide (I). PRO337 polypeptide is useful for detecting PRO4993
CC polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are
CC useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is
CC useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is
CC useful for linking a bioactive molecule to a cell expressing a PRO337
CC polypeptide, and PRO337 is useful for linking a bioactive molecule to a
CC cell expressing a PRO4993 polypeptide. PRO1559 is useful for linking a
CC bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739

Query Match 48.8%; Score 148; DB 6; Length 985;
Best Local Similarity 100.0%; Pred. No. 3.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
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Db          33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy         115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy         175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
               ||||||||||||||||||||||||||||
Db         153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
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RESULT 12
ABO19673
ID ABO19673 standard; protein; 985 AA.
XX
AC ABO19673;
XX
DT 08-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO860.
XX
KW Human; secreted and transmembrane protein; PRO; cell death; neuropathy;
KW peripheral neuropathy; diabetic peripheral neuropathy;
KW AIDS-associated neuropathy; Charcot-Marie-Tooth disease;
KW Refusum's disease; Abetalipoproteinaemia; Tangier disease;
KW Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease;
KW Dejerine-Sottas syndrome; chromosome mapping; gene mapping; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003050240-A1.
XX
PD 13-MAR-2003.
XX
PF 16-OCT-2001; 2001US-00978403.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
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PR 20-MAR-1998; 98US-0078939P.
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PR 21-APR-1998; 98US-0082568P.
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PR 07-MAY-1998; 98US-0084627P.
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PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WL;
XX
DR WPI; 2003-503575/47.
DR N-PSDB; ACD29783.
XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
PS Claim 12; Fig 77; 459pp; English.
XX
CC The invention describes an isolated, secreted and transmembrane
CC polypeptide, termed PRO polypeptide (I). (I) is useful for detecting
CC PRO4993, PRO337, PRO1559, PRO725, PRO700 or PRO739 polypeptide, and for
CC linking a bioactive molecule to a cell expressing the above polypeptides.
CC The bioactive molecule is a toxin, radiolabel or an antibody and causes
CC cell death. (I) is useful as therapeutic agent, in medical and industrial
CC applications e.g. for treating neuropathy, especially peripheral
CC neuropathy, diabetic peripheral neuropathy, AIDS-associated neuropathy,
CC Charcot-Marie-Tooth disease, Refusum's disease, Abetalipoproteinaemia,
CC Tangier disease, Krabbe's disease, Metachromatic leukodystrophy, Fabry's

Query Match 48.8%; Score 148; DB 6; Length 985;
Best Local Similarity 100.0%; Pred. No. 3.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
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Qy 175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
Db 153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180

RESULT 13
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ID ADA12411 standard; protein; 985 AA.
XX
AC ADA12411;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human secreted/transmembrane polypeptide PRO860.
XX
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defect; premature aging; AIDS; cancer;
KW diabetic complication; tissue typing; human.
XX
OS Homo sapiens.

XX
PN US2003055216-A1.
XX
PD 20-MAR-2003.
XX
PF 17-OCT-2001; 2001US-00978824.
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PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

Query Match 48.8%; Score 148; DB 6; Length 985;
Best Local Similarity 100.0%; Pred. No. 3.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
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ID ABO19564 standard; protein; 985 AA.
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AC ABO19564;
XX
DT 27-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane polypeptide #32.
XX
KW Human; secreted and transmembrane protein; PRO; viral infection;
KW tumour growth; retinal disorder; injury; sight loss;
KW retinitis pigmentosum; age-related macular degeneration;
KW sport-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; wound healing; obesity; diabetes; insulinaemia;
KW kidney disorder; mesangial cell function; Berger disease; nephropathy;
KW celiac disease; dermatitis; Crohn disease; neuropathy;
KW cardiac- insufficiency disorder; peripheral neuropathy;
KW diabetic peripheral neuropathy; autonomic neuropathy;
KW reduced motility of the gastrointestinal tract;
KW atony of the urinary bladder; post polio syndrome; Krabbe's disease;
KW Charcot-Marie-Tooth disease; Fabry's disease; Tangier disease;
KW Refsum's disease.
XX
OS Homo sapiens.
XX
PN US2003049633-A1.
XX
PD 13-MAR-2003.
XX
PF 16-OCT-2001; 2001US-00978585.
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PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 16-JUN-1999; 99US-0139557P.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.

Query Match 48.8%; Score 148; DB 6; Length 985;
Best Local Similarity 100.0%; Pred. No. 3.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         33 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 92

Qy        115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
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Db         93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy        175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
              ||||||||||||||||||||||||||||
Db        153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
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RESULT 15
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ID ADB73717 standard; protein; 985 AA.
XX
AC ADB73717;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human PRO polypeptide #32.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein;
KW cell death; neuropathy; neuropathy related disease;
KW Charcot-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;

KW chromosome mapping; gene mapping; genetic disorder; septic shock;
KW antibacterial; immunosuppressive; neuroprotective.
XX
OS Homo sapiens.
XX
PN US2003045462-A1.
XX
PD 06-MAR-2003.
XX
PF 16-OCT-2001; 2001US-00978608.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
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PR 28-MAY-1998; 98US-0087208P.
PR 26-JUN-1998; 98US-00105413.
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PR 01-JUL-1998; 98US-0091359P.
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PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98US-00168978.
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PR 02-NOV-1998; 98US-00184216.
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PR 22-DEC-1998; 98US-00218517.
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PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 16-JUN-1999; 99US-0139557P.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 25-AUG-1999; 99US-00380137.
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PR 25-AUG-1999; 99US-00380142.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
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PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
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PR 05-JAN-2000; 2000WO-US000219.
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PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX

Query Match 48.8%; Score 148; DB 7; Length 985;
Best Local Similarity 100.0%; Pred. No. 3.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
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Qy         115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
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Db          93 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 152

Qy         175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
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Db         153 GKPLALQPGRHTVSGGSLLMARAEKSDE 180
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Search completed: February 27, 2004, 19:37:31
Job time : 81 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 29, 2004, 22:51:23 ; Search time 455 Seconds
(without alignments)
2829.020 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 303
Sequence: 1 MGSGGDSLLGGRGSLPLLLL.....SGPRLPREARELRGQRRNTG 303

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 1

Total number of hits satisfying chosen parameters: 6745146

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10047021/runat_20022004_154121_4513/app_query.fasta_1.455
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10047021_@CGN_1_1_470_@runat_20022004_154121_4513 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	300	99.0	1346	2	AAX51721	Aax51721 DNA encod
2	300	99.0	1346	6	ABQ92573	Abq92573 Human sec
3	148	48.8	3267	6	ABN59723	Abn59723 Novel hum
4	148	48.8	3715	6	ABK87137	Abk87137 cDNA huma
5	148	48.8	3716	2	AAZ34069	Aaz34069 Human PRO
6	148	48.8	3716	3	AAC78502	Aac78502 Human PRO
7	148	48.8	3716	7	ACD42602	Acd42602 Novel hum
8	148	48.8	3716	7	ACA63637	Aca63637 Novel hum
9	148	48.8	3716	7	ACA71801	Aca71801 Human sec
10	148	48.8	3716	7	ABX92441	Abx92441 cDNA enco
11	148	48.8	3716	7	ACA66182	Aca66182 Human cDN
12	148	48.8	3716	8	ADA24749	Ada24749 Novel hum
13	148	48.8	3716	8	ACD29783	Acd29783 Novel hum
14	148	48.8	3716	8	ADA12410	Ada12410 Human cDN
15	148	48.8	3716	8	ACD29198	Acd29198 Novel hum
16	148	48.8	3716	9	ADB73716	Adb73716 Human PRO
17	148	48.8	3716	9	ADB76432	Adb76432 Human PRO
18	148	48.8	3716	9	ADC43858	Adc43858 Human cDN
19	148	48.8	3716	9	ADC61618	Adc61618 Human cDN
20	148	48.8	3716	9	ADC63582	Adc63582 Human cDN
21	148	48.8	3716	9	ADC66682	Adc66682 Human cDN
22	148	48.8	3716	9	ADC68806	Adc68806 Human cDN
23	148	48.8	3716	9	ADC62866	Adc62866 Human cDN
24	148	48.8	3716	9	ADC67931	Adc67931 Human cDN
25	148	48.8	3716	9	ADC41251	Adc41251 Human cDN
26	148	48.8	3716	9	ADC67306	Adc67306 Human cDN
27	148	48.8	3716	9	ADC62242	Adc62242 Human cDN
28	148	48.8	3716	9	ADC41875	Adc41875 Human cDN
29	148	48.8	3716	9	ADE49244	Ade49244 Human cDN
30	148	48.8	3716	9	ADE35298	Ade35298 Human cDN
31	148	48.8	3716	9	ADE16412	Ade16412 Human cDN
32	148	48.8	3716	9	ADD73027	Add73027 Human cDN
33	148	48.8	3716	9	ADD72385	Add72385 Human cDN
34	148	48.8	3716	9	ADE17036	Ade17036 Human cDN
35	148	48.8	3716	10	ADE48544	Ade48544 Human cDN
36	148	48.8	3716	10	ADE89645	Ade89645 Human cDN
37	148	48.8	3808	4	AAS01695	Aas01695 Human TAN
38	120	39.6	756	4	AAH08234	Aah08234 Human cDN
39	120	39.6	4262	4	AAH18180	Aah18180 Human cDN
40	120	39.6	4262	5	AAH78073	Aah78073 Nucleotid
41	110	36.3	3042	4	AAS01694	Aas01694 Human TAN
42	40	13.2	232	3	AAZ42889	Aaz42889 Human 5'
43	33	10.9	299	4	AAS35325	Aas35325 Human car
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ALIGNMENTS

RESULT 1
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ID AAX51721 standard; DNA; 1346 BP.
XX
AC AAX51721;
XX
DT 17-JUN-1999 (first entry)
XX
DE DNA encoding a human secreted protein.
XX
KW Human secreted protein; cancer; immune disorder; infection;
KW inflammatory disorder; skin disorder; tumour; atherosclerosis;
KW restenosis; autoimmune disorder; Alzheimer's disease;
KW peripheral neuropathy; trauma; spinal cord injury; allergy;
KW hematopoietic disorder; skeletal disorder; neurological disorder;
KW arthritic disorder; asthma; immunodeficiency disease; AIDS;
KW transplant rejection; ss.
XX
OS Homo sapiens.
XX
PN WO9911293-A1.
XX
PD 11-MAR-1999.
XX
PF 03-SEP-1998; 98WO-US018360.
XX
PR 05-SEP-1997; 97US-0057626P.
PR 05-SEP-1997; 97US-0057663P.
PR 05-SEP-1997; 97US-0057669P.
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PR 12-SEP-1997; 97US-0058973P.

PR 12-SEP-1997; 97US-0058974P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA, Ruben SM, Lafleur DW, Shi Y, Rosen GA, Olsen HS;
PI Ebner R, Brewer LA;
XX
DR WPI; 1999-204988/17.
DR P-PSDB; AAY12934.
XX
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. neurological disorders,
PT tumors, immune disorders, inflammation or hematological disorders.
XX
PS Claim 1; Page 165-166; 215pp; English.
XX
CC AAX51701-55 encode human secreted proteins. The polynucleotides and their
CC corresponding secreted polypeptides are useful for preventing, treating
CC or ameliorating medical conditions, e.g. by protein or gene therapy.
CC Pathological conditions can also be diagnosed by determining the amount
CC of the new polypeptides in a sample or by determining the presence of
CC mutations in the new polynucleotides. Specific uses are described for
CC each polynucleotide, based on which tissues they are most highly
CC expressed in, and include developing products for the diagnosis or
CC treatment of cancer, immune disorders, infection, inflammatory disorders,
CC skin disorders, tumours, atherosclerosis, restenosis, autoimmune
CC disorders, Alzheimer's disease, peripheral neuropathies, trauma, spinal
CC cord injuries, allergy, hematopoietic disorders, skeletal disorders,
CC neurological disorders, arthritic disorders, asthma, immunodeficiency
CC diseases, AIDS and transplant rejection. The polypeptides are also useful
CC for identifying their binding partners
XX
SQ Sequence 1346 BP; 318 A; 379 C; 376 G; 267 T; 0 U; 6 Other;

Alignment Scores:

Pred. No.:	1.76e-263	Length:	1346
Score:	300.00	Matches:	303
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.01%	Indels:	0
DB:	2	Gaps:	0

US-10-047-021-86 (1-303) x AAX51721 (1-1346)

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Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
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Db         91 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCTTAGTCCACCCCCAGGAC 150

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
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Db        151 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCGAGCCTCAGGCCAGCCACCT 210

Qy         61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
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Db        211 CCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACAC 270

Qy         81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 CACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCAC 330

Qy        101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 390

Qy        121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 GGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAG 450

Qy        141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 ATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCG 510

Qy        161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 CCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTC 570

Qy        181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 CAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGT 630

Qy        201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 GACGAANGGACCTACATGTGTGTGGCCACCAACAGCGCAGGACACAGGGAGAGCCGCGCA 690

Qy        221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaVal 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 GCCCGGGTTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTG 750

Qy        241 ArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 CGAATTCAGCTGGAAAATGTGACACTSCTGAACCCGGATCCTGCAGARGGCCCCAAGCCT 810

Qy        261 ArgProAlaValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThr 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 AGACCGGCGGTGTGGCTCARCTGGAARGTCAGTGGCCCTNTGCGCCTGCCCAATCTTACA 870

Qy        281 ArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArgArg 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 CGGCCTTGTTCAGGACCCAGACTGCCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGGAGG 930

Qy        301 AsnThrGly 303
              ||||||||
Db        931 AACACAGGA 939
```

RESULT 2
ABQ92573
ID ABQ92573 standard; cDNA; 1346 BP.
XX
AC ABQ92573;
XX
DT 12-NOV-2002 (first entry)
XX
DE Human secreted protein encoding cDNA SEQ ID NO 31.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN WO200257420-A2.
XX
PD 25-JUL-2002.
XX
PF 17-JAN-2002; 2002WO-US001109.
XX
PR 18-JAN-2001; 2001US-0262066P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA, Ruben SM, Lafleur DW, Shi Y, Rosen CA, Olsen H;
PI Ebner R, Brewer LA;
XX
DR WPI; 2002-599716/64.
DR P-PSDB; ABP62033.
XX
PT New polynucleotides and polypeptides useful for diagnosing, prognosing,

PT treating or preventing e.g. neurodegenerative, central nervous system,
PT autoimmune, respiratory, reproductive, or inflammatory diseases or
PT disorders.
XX
PS Claim 1; Page 713-714; 785pp; English.
XX
CC The invention relates to novel genes (ABQ92553-ABQ92607) and proteins
CC (ABP62013-ABP62153) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections
XX
SQ Sequence 1346 BP; 318 A; 379 C; 376 G; 267 T; 0 U; 6 Other;

Alignment Scores:

Pred. No.:	1.76e-263	Length:	1346
Score:	300.00	Matches:	303
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.01%	Indels:	0
DB:	6	Gaps:	0

US-10-047-021-86 (1-303) x ABQ92573 (1-1346)

```
Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 90

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCTTAGTCCACCCCCAGGAC 150

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCGAGCCTCAGGCCAGCCACCT 210

Qy         61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 CCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACAC 270

Qy         81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 CACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCAC 330

Qy        101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 390

Qy        121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 GGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAG 450

Qy        141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 ATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCG 510

Qy        161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 CCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTC 570

Qy        181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 CAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGT 630

Qy        201 AspGlu***ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAla 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 GACGAANGGACCTACATGTGTGTGGCCACCAACAGCGCAGGACACAGGGAGAGCCGCGCA 690

Qy        221 AlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaVal 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 GCCCGGGTTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTG 750

Qy        241 ArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPro 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 CGAATTCAGCTGGAAAATGTGACACTSCTGAACCCGGATCCTGCAGARGGCCCCAAGCCT 810

Qy        261 ArgProAlaValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThr 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 AGACCGGCGGTGTGGCTCARCTGGAARGTCAGTGGCCCTNTGCGCCTGCCCAATCTTACA 870

Qy        281 ArgProCysSerGlyProArgLeuProArgGluAlaArgGluLeuArgGlyGlnArgArg 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 CGGCCTTGTTCAGGACCCAGACTGCCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGGAGG 930

Qy        301 AsnThrGly 303
              ||||||||
Db        931 AACACAGGA 939
```

RESULT 3
ABN59723
ID ABN59723 standard; cDNA; 3267 BP.
XX
AC ABN59723;
XX
DT 28-JUN-2002 (first entry)
XX
DE Novel human coding sequence SEQ ID NO: 134.
XX
KW Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200222660-A2.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US026015.
XX
PR 11-SEP-2000; 2000US-00659671.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI; 2002-292408/33.
DR P-PSDB; ABB97310.
XX
PT An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis.
XX
PS Claim 1; SEQ ID NO 134; 509pp; English.
XX
CC The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.
CC rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a coding sequence of the

```
CC   invention
XX
SQ   Sequence 3267 BP; 628 A; 1101 C; 927 G; 611 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.23e-124      Length:         3267
Score:                  148.00         Matches:        264
Percent Similarity:     98.51%         Conservative:   0
Best Local Similarity:  98.51%         Mismatches:     2
Query Match:            48.84%         Indels:         4
DB:                     6              Gaps:           0

US-10-047-021-86 (1-303) x ABN59723 (1-3267)

Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 94

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 154

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
              ||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db        155 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACC 213

Qy         60 oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACA 273

Qy         80 sHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 CCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCA 333

Qy        100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CGATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCT 393

Qy        120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TGGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCA 453

Qy        140 nIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 GATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCC 513

Qy        160 oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCT 573

Qy        180 uGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSe 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 CCAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAG 633

Qy        200 rAspGlu***-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgA 220
              |||||||    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 TGACGAAGG-GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCG 692

Qy        220 laAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 CAGCCCGGGTTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTG 752

Qy        240 alArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysP 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 TGCGAATTCAGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGC 812

Qy        260 roArgProAlaValTrpLeu 266
              ||||||||||||||||||
Db        813 CTAGACCGGCGGTGTGGCTC 832

RESULT 4
ABK87137
ID   ABK87137 standard; cDNA; 3715 BP.
XX
AC   ABK87137;
XX
DT   07-OCT-2002  (first entry)
XX
DE   cDNA human ECSM4 protein.
XX
KW   Human; endothelial cell-specific molecule 4; ECSM4; neovasculature;
KW   imaging vascular endothelium; proliferative disease; cancer; psoriasis;
KW   diabetic retinopathy; atherosclerosis; menorrhagia; endothelial damage;
KW   tumour neovasculature; cardiac disease; endometriosis; hypoxic condition;
KW   angiogenesis; cytostatic; cardiant; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             70. .3384
FT                   /*tag=  a
FT                   /product= "ECSM4"
XX
PN   WO200236771-A2.
XX
PD   10-MAY-2002.
XX
PF   06-NOV-2001; 2001WO-GB004906.
XX
PR   06-NOV-2000; 2000US-0245566P.
PR   07-MAR-2001; 2001US-0273662P.
XX
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX
PI   Bicknell R,  Huminiecki L;
XX
DR   WPI; 2002-508120/54.
DR   P-PSDB; AAU99419.
XX
PT   Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for
PT   imaging, diagnosing and treating a condition involving vascular
PT   endothelium e.g. cancer, cardiac disease, endometriosis, diabetes.
XX
PS   Disclosure; Fig 12; 248pp; English.
XX
CC   The present invention relates to endothelial cell-specific molecule 4
CC   (ECSM4), and the polynucleotide sequences encoding it. The ECSM4 proteins
CC   are useful for imaging vascular endothelium in the body of an individual,
CC   and for diagnosing and treating a proliferative disease or condition
CC   involving the vascular endothelium (preferably, neovasculature) such as
CC   cancer, psoriasis, diabetic retinopathy, atherosclerosis or menorrhagia.
CC   The ECSM4 proteins are also useful in the manufacture of diagnostic or
CC   prognostic agent for such conditions. The proteins are also useful for
CC   detecting endothelial damage or activation, detecting a tumour or tumour
CC   neovasculature, cardiac disease, or endometriosis by detecting the amount
CC   of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4
CC   are useful in gene therapy for treating a hypoxic condition such as
CC   cancer, cardiac disease, endometriosis or atherosclerosis and in the
CC   manufacture of medicaments for treating the above disease. The sequences
CC   are useful for modulating angiogenesis in an individual. The present
CC   sequence encodes human ECSM4 protein
XX
SQ   Sequence 3715 BP; 725 A; 1239 C; 1053 G; 698 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.39e-124      Length:         3715
Score:                  148.00         Matches:        264
Percent Similarity:     98.51%         Conservative:   0
Best Local Similarity:  98.51%         Mismatches:     2
Query Match:            48.84%         Indels:         4
DB:                     6              Gaps:           0

US-10-047-021-86 (1-303) x ABK87137 (1-3715)

Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         70 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 129

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp  40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 189

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr  60
              ||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db        190 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACC 248

Qy         60 oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi  80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 TCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACA 308

Qy         80 sHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCA 368

Qy        100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CGATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCT 428

Qy        120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TGGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCA 488

Qy        140 nIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 GATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCC 548

Qy        160 oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 GCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCT 608

Qy        180 uGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSe 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CCAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAG 668

Qy        200 rAspGlu***-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgA 220
              |||||||    ||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 TGACGAAGG-GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCG 727

Qy        220 laAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 CAGCCCGGGTTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTG 787

Qy        240 alArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysP 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 TGCGAATTCAGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGC 847

Qy        260 roArgProAlaValTrpLeu 266
              |||||||||||||||||||
Db        848 CTAGACCGGCGGTGTGGCTC 867
```

RESULT 5
AAZ34069
ID AAZ34069 standard; cDNA; 3716 BP.
XX
AC AAZ34069;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO860 nucleotide sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US005028.
XX
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
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PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
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PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
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PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
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PR 28-APR-1998; 98US-0083322P.
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PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
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PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
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PR   28-MAY-1998;   98US-0087106P.
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PR   30-JUL-1998;   98US-0094651P.
PR   11-SEP-1998;   98US-0100038P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Wood WI,  Goddard A,  Gurney A,  Yuan J,  Baker KP,  Chen J;
XX
DR   WPI; 1999-551358/46.
DR   P-PSDB; AAY41716.
XX
PT   New secreted and transmembrane polypeptides and their polynucleotides,
PT   useful for treating blood coagulation disorders, cancers and cellular
PT   adhesion disorders.
XX
PS   Claim 2; Fig 76; 530pp; English.
XX
CC   The present invention describes secreted and transmembrane polypeptides
CC   and their polynucleotides. The nucleotide sequences are useful as sources
CC   of probes, primers, for chromosome mapping, and for generation of
CC   antisense sequences. They can also be used to create transgenic animals.
CC   The proteins can be used to treat a variety of diseases and disorders,
CC   depending on their function. Diseases that may be treated include blood
CC   coagulation disorders, cancers and cellular adhesion disorders. They may
CC   also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
CC   AAY41774 represent polynucleotide and polypeptide sequence given in the
CC   exemplification of the present invention
XX
SQ   Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.39e-124      Length:          3716
Score:                    148.00         Matches:         261
Percent Similarity:       98.49%         Conservative:    0
Best Local Similarity:    98.49%         Mismatches:      2
Query Match:              48.84%         Indels:          4
DB:                       2              Gaps:            0

US-10-047-021-86 (1-303) x AAZ34069 (1-3716)

Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuIleMet 23
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Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
              |||||||||||||||||||||||||||||||    |||||||||||||||||||||||||
Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 239

Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
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Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
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Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
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Db        480 CCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539

Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
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Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
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Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
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Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
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Db        779 CGGTGTGGCTC 789

RESULT 6
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ID   AAC78502 standard; cDNA; 3716 BP.
XX
AC   AAC78502;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human PRO860 (UNQ421) nucleotide sequence SEQ ID NO:210.
XX
KW   Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW   expressed sequence tag; detection; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200053756-A2.
XX
PD   14-SEP-2000.
XX
PF   18-FEB-2000; 2000WO-US004341.
XX
PR   08-MAR-1999;   99WO-US005028.
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PR   29-MAR-1999;   99US-0126773P.
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PR   26-JUL-1999;   99US-0145698P.
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PR   30-NOV-1999;   99WO-US028313.
PR   02-DEC-1999;   99WO-US028551.
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PR   16-DEC-1999;   99WO-US030095.
PR   30-DEC-1999;   99WO-US031243.
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PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
DR P-PSDB; AAB44272.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX
PS Claim 2; Fig 76; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytostatic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX
SQ Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.39e-124	Length:	3716
Score:	148.00	Matches:	261
Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
Query Match:	48.84%	Indels:	4
DB:	3	Gaps:	0

US-10-047-021-86 (1-303) x AAC78502 (1-3716)

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Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuIleMet 23
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
              |||||||||||||||||||||||||||||||    |||||||||||||||||||||||||||
Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
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Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
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Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
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Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
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Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539

Qy        183 yArgHisThrValSerGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
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Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
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Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
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Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
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Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
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Db        779 CGGTGTGGCTC 789
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RESULT 7
ACD42602
ID ACD42602 standard; cDNA; 3716 BP.
XX
AC ACD42602;
XX
DT 09-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO860 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; virucide; gene therapy;
KW cell death; growth induction cascade; blood coagulation cascade;
KW viral infection; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003050239-A1.
XX
PD 13-MAR-2003.
XX
PF 15-OCT-2001; 2001US-00978191.
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PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
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PR 14-MAY-1999; 99US-00311832.
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PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
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PR 16-DEC-1999; 99WO-US030095.
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PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.

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PR   05-JUN-2001; 2001US-00874503.
PR   14-JUN-2001; 2001US-00882636.
PR   19-JUN-2001; 2001US-00886342.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   30-JUL-2001; 2001US-00918585.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME;

Alignment Scores:
Pred. No.:              1.39e-124       Length:         3716
Score:                  148.00          Matches:        261
Percent Similarity:     98.49%          Conservative:   0
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DB:                     7               Gaps:           0

US-10-047-021-86 (1-303) x ACD42602 (1-3716)

Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuIleMet 23
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Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
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Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
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Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
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Db        180 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 239

Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
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Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
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Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
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Qy        143 cArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
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Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
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Db        480 CCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539

Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
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Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
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Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 TTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTC 718

Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
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Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
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Db        779 CGGTGTGGCTC 789

RESULT 8
ACA63637
ID   ACA63637 standard; cDNA; 3716 BP.
XX
AC   ACA63637;
XX
DT   16-JUN-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO860 cDNA.
XX
KW   Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW   antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW   antidiabetic; gene therapy; inflammatory disease; organ failure;
KW   atherosclerosis; cardiac injury; infertility; birth defect;
KW   premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
KW   gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
KW   tissue typing; gene; ss.
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OS   Homo sapiens.
XX
PN   US2002192706-A1.
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PD   19-DEC-2002.
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PF   24-OCT-2001; 2001US-00999832.
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PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98WO-US024855.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
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PR 14-MAY-1999; 99WO-US010733.
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PR 30-NOV-1999; 99WO-US028313.
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PR 30-DEC-1999; 99WO-US031243.
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PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-328860/31.
DR P-PSDB; ABU72224.
XX
PT New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
PS Claim 2; Fig 76; 453pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC is at least 80 % sequence identity to, or the full-length coding sequence
CC of, any of 118 300-2100 nucleotide sequences, which encodes its
CC corresponding PRO polypeptide selected from 118 100-700 amino acid
CC sequences, all given in the specification. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS, cancer, or diabetic complications. The nucleic
CC acids are useful as hybridisation probes, in chromosome and gene mapping,
CC and in generating antisense RNA or DNA. The polypeptides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
CC in tissue typing. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.39e-124	Length:	3716
Score:	148.00	Matches:	261
Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
Query Match:	48.84%	Indels:	4
DB:	7	Gaps:	0

US-10-047-021-86 (1-303) x ACA63637 (1-3716)

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Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuIleMet 23
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Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
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Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
              |||||||||||||||||||||||||||||||    |||||||||||||||||||||||||||
Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
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Db        180 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 239

Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
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Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
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Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
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Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539

Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
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Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
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Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
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Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
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Qy        263 laValTrpLeu 266
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Db        779 CGGTGTGGCTC 789

RESULT 9
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ID   ACA71801 standard; cDNA; 3716 BP.
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AC   ACA71801;
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DT   11-AUG-2003  (first entry)
XX
DE   Human secreted and transmembrane polypeptide PRO860 cDNA.
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KW   Human; ss; gene; thrombolytic agent; interferon; interleukin; cytokine;
KW   erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;
KW   apoptosis related condition; AIDS; amyotrophic lateral sclerosis;
KW   inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;
KW   gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;
KW   hypertension; myocardial ischaemia; kidney disease; carcinogenesis;
KW   glomerulonephritis; lung disease; pulmonary hypertension; preeclampsia;
KW   bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;
KW   inflammatory bowel disease; reproductive disorder; premature labour.
XX
OS   Homo sapiens.
XX
PN   US2002177553-A1.
XX
PD   28-NOV-2002.
XX
PF   15-OCT-2001; 2001US-00978192.
XX
PR   17-OCT-1997;   97US-0062250P.
PR   03-NOV-1997;   97US-0064249P.
PR   13-NOV-1997;   97US-0065311P.
PR   21-NOV-1997;   97US-0066364P.
PR   10-MAR-1998;   98US-0077450P.
PR   11-MAR-1998;   98US-0077632P.
PR   11-MAR-1998;   98US-0077641P.
PR   11-MAR-1998;   98US-0077649P.
PR   12-MAR-1998;   98US-0077791P.
PR   13-MAR-1998;   98US-0078004P.
PR   17-MAR-1998;   98US-00040220.
PR   20-MAR-1998;   98US-0078886P.
PR   20-MAR-1998;   98US-0078910P.
PR   20-MAR-1998;   98US-0078936P.
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PR   27-MAR-1998;   98US-0079689P.
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PR   25-MAY-2001; 2001WO-US017092.
PR   01-JUN-2001; 2001US-00872035.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   14-JUN-2001; 2001US-00882636.
PR   19-JUN-2001; 2001US-00886342.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   30-JUL-2001; 2001US-00918585.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI   Kljavin IJ,  Kuo SS,  Napier MA,  Pan J,  Paoni NF,  Roy MA,  Shelton DL;
PI   Stewart TA,  Tumas D,  Williams PM,  Wood WI;
XX
DR   WPI; 2003-328499/31.
DR   P-PSDB; ABU84904.
XX
PT   New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
PT   pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
PT   modulators of receptor-ligand interactions.
XX
PS   Claim 2; SEQ ID NO 210; 55pp; English.
XX
CC   The invention relates to an isolated secreted and transmembrane
CC   polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
CC   in PRO polypeptide detection methods. The PRO polypeptide is useful for
CC   linking a bioactive molecule to a cell. The PRO polypeptide or an
CC   antibody against it is useful for modulating a biological activity of a
CC   cell. The PRO polypeptide is useful in industrial applications including
CC   pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
CC   polypeptide is also useful as a thrombolytic agent, interferon,
CC   interleukin, erythropoietin, colony stimulating factor and other
CC   cytokines. The PRO polypeptide is useful for treating disease such as
```

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CC   cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,
CC   amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,
CC   atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
CC   Parkinson's disease; cardiovascular disease e.g. hypertension and
CC   myocardial ischaemia; kidney disease e.g. renal failure and
CC   glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
CC   asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory
CC   bowel disease; reproductive disorders e.g. premature labour and
CC   preeclampsia; carcinogenesis. The present sequence represents a cDNA
CC   encoding a PRO polypeptide of the invention. Note: The sequence data for
CC   this patent did not form part of the printed specification but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20020177553
XX
SQ   Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.39e-124       Length:         3716
Score:                  148.00          Matches:        261
Percent Similarity:     98.49%          Conservative:   0
Best Local Similarity:  98.49%          Mismatches:     2
Query Match:            48.84%          Indels:         4
DB:                     7               Gaps:           0

US-10-047-021-86 (1-303) x ACA71801 (1-3716)

Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuIleMet 23
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Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
              |||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 239

Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539

Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 TTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTC 718

Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
              |||||||||
Db        779 CGGTGTGGCTC 789

RESULT 10
ABX92441
ID   ABX92441 standard; cDNA; 3716 BP.
XX
AC   ABX92441;
XX
DT   08-MAY-2003  (first entry)
XX
DE   cDNA encoding human PRO860 polypeptide.
XX
KW   Human; PRO polypeptide; secreted and transmembrane protein;
KW   immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW   cardiac insufficiency; nervous system disorder; kidney disorder;
KW   bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW   genetic disorder; cytostatic; antidiabetic; antiinflammatory;
KW   antiarthritic; anti-tumour; vulnerary; antianaemic; dermatological;
KW   cardiant; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2002169284-A1.
XX
PD   14-NOV-2002.
XX
PF   16-OCT-2001; 2001US-00978697.
XX
PR   26-MAY-1981;   81US-00267213.
PR   17-OCT-1997;   97US-0062250P.
PR   03-NOV-1997;   97US-0064249P.
PR   13-NOV-1997;   97US-0065311P.
PR   21-NOV-1997;   97US-0066364P.
PR   10-MAR-1998;   98US-0077450P.
PR   11-MAR-1998;   98US-0077632P.
PR   11-MAR-1998;   98US-0077641P.
PR   11-MAR-1998;   98US-0077649P.
PR   12-MAR-1998;   98US-0077791P.
PR   13-MAR-1998;   98US-0078004P.
PR   17-MAR-1998;   98US-00040220.
PR   20-MAR-1998;   98US-0078886P.
PR   20-MAR-1998;   98US-0078910P.
PR   20-MAR-1998;   98US-0078936P.
PR   20-MAR-1998;   98US-0078939P.
PR   25-MAR-1998;   98US-0079294P.
PR   26-MAR-1998;   98US-0079656P.
PR   27-MAR-1998;   98US-0079663P.
PR   27-MAR-1998;   98US-0079664P.
PR   27-MAR-1998;   98US-0079689P.
PR   27-MAR-1998;   98US-0079728P.
PR   27-MAR-1998;   98US-0079786P.
PR   30-MAR-1998;   98US-0079920P.
PR   30-MAR-1998;   98US-0079923P.
PR   26-JUN-1998;   98US-00105413.
PR   07-OCT-1998;   98US-00168978.
PR   07-OCT-1998;   98WO-US021141.
PR   02-NOV-1998;   98US-00184216.
PR   06-NOV-1998;   98US-00187368.
PR   20-NOV-1998;   98WO-US024855.
PR   07-DEC-1998;   98US-00202054.
PR   22-DEC-1998;   98US-00218517.
PR   05-JAN-1999;   99WO-US000106.
PR   05-MAR-1999;   99US-00254465.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99US-00265686.
PR   10-MAR-1999;   99WO-US005190.
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PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-288163/28.
DR P-PSDB; ABU61102.
XX
PT Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies.
XX
PS Claim 2; Fig 76; 459pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The bioactive molecule maybe a
CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.
CC The PRO polypeptides are useful for treating immune disorders, diabetes
CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system
CC disorders, kidney disorders, bone and cartilage disorders or arthritis,
CC tumours, and wound healing. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and gene
CC mapping, in the generation of antisense RNA and DNA, in the preparation
CC of PRO polypeptides, for generating transgenic animals or knockout
CC animals, for the genetic analysis of individuals with genetic disorders,
CC and in gene therapy. The present sequence encodes a human PRO polypeptide
CC of the invention. Note: The sequence data for this patent was obtained in
CC electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.39e-124	Length:	3716
Score:	148.00	Matches:	261
Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
Query Match:	48.84%	Indels:	4
DB:	7	Gaps:	0

US-10-047-021-86 (1-303) x ABX92441 (1-3716)

```
Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuIleMet 23
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 239

Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539

Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
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Db        659 TTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTC 718

Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
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Db        779 CGGTGTGGCTC 789

RESULT 11
ACA66182
ID   ACA66182 standard; cDNA; 3716 BP.
XX
AC   ACA66182;
XX
DT   24-JUN-2003  (first entry)
XX
DE   Human cDNA encoding secreted/transmembrane protein PRO860.
XX
KW   Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW   malignancy; cancer; ovarian cancer; colorectal cancer; sarcoma;
KW   leukaemia; lymphoma; inflammatory disease; necrosis; atherosclerosis;
KW   infertility; premature aging; psoriasis; inflammatory disease;
KW   renal disease; arthritis; immune-mediated alopecia; stroke; encephalitis;
KW   hepatitis; multiple sclerosis; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2003004102-A1.
XX
PD   02-JAN-2003.
XX
PF   15-OCT-2001; 2001US-00978189.
XX
PR   17-OCT-1997;   97US-0062250P.
PR   03-NOV-1997;   97US-0064249P.
PR   13-NOV-1997;   97US-0065311P.
PR   21-NOV-1997;   97US-0066364P.
PR   10-MAR-1998;   98US-0077450P.
PR   11-MAR-1998;   98US-0077632P.
PR   11-MAR-1998;   98US-0077641P.
PR   11-MAR-1998;   98US-0077649P.
PR   12-MAR-1998;   98US-0077791P.
PR   13-MAR-1998;   98US-0078004P.
PR   17-MAR-1998;   98US-00040220.
PR   20-MAR-1998;   98US-0078886P.
PR   20-MAR-1998;   98US-0078910P.
PR   20-MAR-1998;   98US-0078936P.
PR   20-MAR-1998;   98US-0078939P.
PR   25-MAR-1998;   98US-0079294P.
PR   26-MAR-1998;   98US-0079656P.
PR   27-MAR-1998;   98US-0079663P.
PR   27-MAR-1998;   98US-0079664P.
PR   27-MAR-1998;   98US-0079689P.
PR   27-MAR-1998;   98US-0079728P.
PR   27-MAR-1998;   98US-0079786P.
PR   30-MAR-1998;   98US-0079920P.
PR   30-MAR-1998;   98US-0079923P.
PR   26-JUN-1998;   98US-00105413.
PR   07-OCT-1998;   98US-00168978.
PR   07-OCT-1998;   98WO-US021141.
PR   02-NOV-1998;   98US-00184216.
PR   06-NOV-1998;   98US-00187368.
PR   20-NOV-1998;   98WO-US024855.
PR   07-DEC-1998;   98US-00202054.
PR   22-DEC-1998;   98US-00218517.
PR   05-JAN-1999;   99WO-US000106.
PR   05-MAR-1999;   99US-00254465.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99US-00265686.
PR   10-MAR-1999;   99WO-US005190.
PR   12-MAR-1999;   99US-00267213.
PR   12-APR-1999;   99US-00284291.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   25-AUG-1999;   99US-00380137.
PR   25-AUG-1999;   99US-00380138.
PR   25-AUG-1999;   99US-00380142.
PR   30-NOV-1999;   99WO-US028313.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000US-00709238.
PR   10-NOV-2000; 2000WO-US030873.
PR   27-NOV-2000; 2000US-00723749.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   22-MAR-2001; 2001US-00816920.
PR   22-MAR-2001; 2001WO-US009552.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   25-MAY-2001; 2001WO-US017092.
PR   01-JUN-2001; 2001US-00872035.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   14-JUN-2001; 2001US-00882636.
PR   19-JUN-2001; 2001US-00886342.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   30-JUL-2001; 2001US-00918585.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI   Kljavin IJ,  Kuo SS,  Napier MA,  Pan J,  Paoni NF,  Roy MA,  Shelton DL;
PI   Stewart TA,  Tumas D,  Williams PM,  Wood WI;
XX
DR   WPI; 2003-341189/32.
DR   P-PSDB; ABU80371.
XX
PT   New genes and secreted and transmembrane polypeptides (e.g. PRO337 or
PT   PRO1559), useful for treating or diagnosing e.g. cancers,
PT   atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple
PT   sclerosis in mammals.
XX
PS   Claim 2; Fig 76; 460pp; English.
XX
CC   The invention relates to a new isolated nucleic acid molecule comprises a
```

```
CC   sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC   94 PRO polypeptides whose sequences are fully defined in the
CC   specification; or (b) any of 94 nucleotide sequences fully defined in the
CC   specification; or the full length coding sequence of any these 94
CC   nucleotide sequences. Also included are an isolated PRO polypeptide
CC   scoring at least 80% positives when compared to any of the PRO
CC   polypeptide sequences cited above (or an isolated PRO polypeptide having
CC   at least 80% amino acid sequence identity to: (a) an amino acid sequence
CC   encoded by the nucleotide deposited with ATCC numbers listed in the
CC   specification; (b) the PRO polypeptide, lacking its associated signal
CC   peptide; or (c) an extracellular domain of the PRO polypeptide, with or
CC   lacking its associated signal peptide), a vector comprising the nucleic
CC   acid molecule, a host cell comprising the vector (and producing a PRO
CC   polypeptide), a chimaeric molecule comprising the PRO polypeptide fused
CC   to a heterologous amino acid sequence and an anti-PRO antibody. The PRO
CC   polypeptides or polynucleotides are useful as pharmaceuticals,
CC   diagnostics, biosensors or bioreactors. These are particularly useful for
CC   detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,
CC   colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease,
CC   necrosis, atherosclerosis, infertility, premature aging, psoriasis,
CC   inflammatory disease, renal disease, arthritis, immune-mediated alopecia,
CC   stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The
CC   PRO polypeptides are useful in drug screening, particularly as targets
CC   for therapeutic intervention in these diseases, and in the diagnostic
CC   determination of the presence of these diseases. The PRO polypeptides are
CC   also useful as molecular weight markers, or for chromosome
CC   identification. The PRO genes are useful as hybridisation probes, or for
CC   screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC   also be used in gene therapy, particularly for replacing a defective
CC   gene. The present sequence encodes a PRO polypeptide
XX
SQ   Sequence 3716 BP; 757 A; 1225 C; 1032 G; 702 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.39e-124       Length:          3716
Score:                    148.00          Matches:         261
Percent Similarity:       98.49%          Conservative:    0
Best Local Similarity:    98.49%          Mismatches:      2
Query Match:              48.84%          Indels:          4
DB:                       7               Gaps:            0

US-10-047-021-86 (1-303) x ACA66182 (1-3716)

Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuIleMet 23
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
              ||||||||||||||||||||||||||||||    |||||||||||||||||||||||||
Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 239

Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
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Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
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Db        480 CCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539

Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
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Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
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Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
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Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
              ||||||||||
Db        779 CGGTGTGGCTC 789
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RESULT 12
ADA24749
ID ADA24749 standard; cDNA; 3716 BP.
XX
AC ADA24749;
XX
DT 20-NOV-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO860 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; gene; ss; tissue typing;
KW chromosome identification; vaccine; cancer; retinal disorder;
KW sports-related joint disorder; osteoarthritis; rheumatoid arthritis;
KW wound healing; obesity; diabetes; hearing loss;
KW cardiac insufficiency disorder; kidney disorder; nervous system disorder;
KW haemoglobin associated disorder.
XX
OS Homo sapiens.
XX
PN US2003050241-A1.
XX
PD 13-MAR-2003.
XX
PF 16-OCT-2001; 2001US-00978564.
XX
PR 17-OCT-1997; 97US-0062250P.
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PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98US-0109304P.
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PR 22-DEC-1998; 98US-0113296P.
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PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
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PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 16-JUN-1999; 99US-0139557P.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-521814/49.
DR P-PSDB; ADA24750.
XX
PT New isolated PRO polypeptides for example extracellular, secreted and
PT membrane bound proteins, useful for modulating the biological activities
PT of cells and for treating, for example diabetes, cancer, rheumatoid
PT arthritis, and hearing loss.
XX
PS Claim 2; Fig 76; 461pp; English.
XX

CC The invention describes an isolated secreted and transmembrane (PRO)
CC polypeptide (I). PRO337 polypeptide is useful for detecting PRO4993
CC polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are
CC useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is
CC useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is
CC useful for linking a bioactive molecule to a cell expressing a PRO337
CC polypeptide, and PRO337 is useful for linking a bioactive molecule to a
CC cell expressing a PRO4993 polypeptide. PRO1559 is useful for linking a
CC bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739

Alignment Scores:

Pred. No.:	1.39e-124	Length:	3716
Score:	148.00	Matches:	261
Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
Query Match:	48.84%	Indels:	4
DB:	8	Gaps:	0

US-10-047-021-86 (1-303) x ADA24749 (1-3716)

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Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuIleMet 23
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Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
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Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
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Qy         83 uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
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Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
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Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
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Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
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Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
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Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
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Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 TTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTC 718

Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
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Db        779 CGGTGTGGCTC 789
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RESULT 13
ACD29783
ID ACD29783 standard; cDNA; 3716 BP.
XX
AC ACD29783;
XX
DT 08-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO860 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; cell death; neuropathy;
KW peripheral neuropathy; diabetic peripheral neuropathy;
KW AIDS-associated neuropathy; Charcot-Marie-Tooth disease;
KW Refusum's disease; Abetalipoproteinaemia; Tangier disease;
KW Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease;
KW Dejerine-Sottas syndrome; chromosome mapping; gene mapping; gene therapy;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN US2003050240-A1.
XX
PD 13-MAR-2003.
XX
PF 16-OCT-2001; 2001US-00978403.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
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PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
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PA (GETH) GENENTECH INC.
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PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WL;
XX
DR WPI; 2003-503575/47.
DR P-PSDB; ABO19673.
XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
PS Claim 2; Fig 76; 459pp; English.
XX
CC The invention describes an isolated, secreted and transmembrane
CC polypeptide, termed PRO polypeptide (I). (I) is useful for detecting
CC PRO4993, PRO337, PRO1559, PRO725, PRO700 or PRO739 polypeptide, and for
CC linking a bioactive molecule to a cell expressing the above polypeptides.
CC The bioactive molecule is a toxin, radiolabel or an antibody and causes
CC cell death. (I) is useful as therapeutic agent, in medical and industrial
CC applications e.g. for treating neuropathy, especially peripheral
CC neuropathy, diabetic peripheral neuropathy, AIDS-associated neuropathy,
CC Charcot-Marie-Tooth disease, Refusum's disease, Abetalipoproteinaemia,

Alignment Scores:

Pred. No.:	1.39e-124	Length:	3716
Score:	148.00	Matches:	261
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Best Local Similarity:	98.49%	Mismatches:	2
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US-10-047-021-86 (1-303) x ACD29783 (1-3716)

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KW cardiac injury; infertility; birth defect; premature aging; AIDS; cancer;
KW diabetic complication; tissue typing; human.
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OS Homo sapiens.
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PN US2003055216-A1.
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XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

Alignment Scores:

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Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
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US-10-047-021-86 (1-303) x ADA12410 (1-3716)

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DT   27-AUG-2003  (first entry)
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KW   retinitis pigmentosum; age-related macular degeneration;
KW   sport-related joint problem; articular cartilage defect; osteoarthritis;
KW   rheumatoid arthritis; wound healing; obesity; diabetes; insulinaemia;
KW   kidney disorder; mesangial cell function; Berger disease; nephropathy;
KW   celiac disease; dermatitis; Crohn disease; neuropathy;
KW   cardiac- insufficiency disorder; peripheral neuropathy;
KW   diabetic peripheral neuropathy; autonomic neuropathy;
KW   reduced motility of the gastrointestinal tract;
KW   atony of the urinary bladder; post polio syndrome; Krabbe's disease;
KW   Charcot-Marie-Tooth disease; Fabry's disease; Tangier disease;
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GenCore version 5.1.6
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; APPLICANT: Mark P. Roach
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; CURRENT FILING DATE: 2001-12-18
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;   NAME/KEY: misc_feature
;   LOCATION: (174657)...(174756)
;   OTHER INFORMATION: n = A,T,C or G
;   NAME/KEY: misc_feature
;   LOCATION: (186224)...(186323)
;   OTHER INFORMATION: n = A,T,C or G
;   NAME/KEY: misc_feature
;   LOCATION: (195242)...(195341)
;   OTHER INFORMATION: n = A,T,C or G
;   NAME/KEY: unsure
;   LOCATION: 202703
;   OTHER INFORMATION: unknown
;   NAME/KEY: misc_feature
;   LOCATION: (202771)...(202870)
;   OTHER INFORMATION: n = A,T,C or G
;   NAME/KEY: misc_feature
;   LOCATION: (206246)...(215602)
;   OTHER INFORMATION: n = A,T,C or G
;   NAME/KEY: misc_feature
;   LOCATION: (218126)...(218225)
;   OTHER INFORMATION: n = A,T,C or G
;   NAME/KEY: misc_feature
;   LOCATION: (220360)...(220459)
;   OTHER INFORMATION: n = A,T,C or G
;   NAME/KEY: misc_feature
;   LOCATION: (222717)...(222816)
;   OTHER INFORMATION: n = A,T,C or G
;   NAME/KEY: misc_feature
;   LOCATION: (223981)...(224080)
;   OTHER INFORMATION: n = A,T,C or G
;   NAME/KEY: misc_feature
;   LOCATION: (227487)...(227586)
;   OTHER INFORMATION: n = A,T,C or G
;   NAME/KEY: misc_feature
;   LOCATION: (230157)...(230256)
;   OTHER INFORMATION: n = A,T,C or G
;   NAME/KEY: misc_feature
;   LOCATION: (232299)...(232398)
;   OTHER INFORMATION: n = A,T,C or G
;   NAME/KEY: misc_feature
;   LOCATION: (236552)...(2366651)
;   OTHER INFORMATION: n = A,T,C or G
;   NAME/KEY: misc_feature
;   LOCATION: (238789)...(248788)
;   OTHER INFORMATION: n = A,T,C or G
;   NAME/KEY: exon
;   LOCATION: (118288)...(119101)
;   OTHER INFORMATION: exon 1C
;   NAME/KEY: exon:intron junction
;   LOCATION: (151129)...(151130)
;   OTHER INFORMATION: exon 5:intron 5
;   NAME/KEY: exon:intron junction
;   LOCATION: (299248)...(299249)
;   OTHER INFORMATION: exon 9:intron 9
;   NAME/KEY: exon:intron junction
;   LOCATION: (348578)...(348579)
;   OTHER INFORMATION: exon 10:intron 10
;   NAME/KEY: intron
;   LOCATION: (348579)...(381838)
;   OTHER INFORMATION: intron 10
;   NAME/KEY: intron:exon junction
;   LOCATION: (386185)...(386186)
;   OTHER INFORMATION: intron 11:exon 12
US-10-027-983-11

Alignment Scores:
Pred. No.:              7.57e+03        Length:         392000
Score                   9.00            Matches         9
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            2.97%           Indels:         0
DB:                     4               Gaps:           0

US-10-047-021-86 (1-303) x US-10-027-983-11 (1-392000)

Qy          14 SerLeuProLeuLeuLeuLeuIle 22
               |||||||||||||||||||||||||
Db      250555 TCCCTTCCTTTGCTCTTGCTCTTGATT 250581

RESULT 2
US-09-016-434-278/c
; Sequence 278, Application US/09016434
; Patent No. 6500938
;  GENERAL INFORMATION:
;    APPLICANT:  Janice Au-Young
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;    TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;    NUMBER OF SEQUENCES:  1490
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  278:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  280 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  UCMCNOT02
;      CLONE:  1714778
US-09-016-434-278

Alignment Scores:
Pred. No.:              63.7            Length:         280
Score:                  8.00            Matches:        8
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            2.64%           Indels:         0
DB:                     4               Gaps:           0

US-10-047-021-86 (1-303) x US-09-016-434-278 (1-280)

Qy          16 ProLeuLeuLeuLeuLeuIleMet 23
               |||||||||||||||||||||||
Db         140 CCTCTTCTGCTTCTCTTAATAATG 117
```

```
RESULT 3
US-09-173-151A-5/c
; Sequence 5, Application US/09173151A
; Patent No. 6326472
;  GENERAL INFORMATION:
;    APPLICANT:  Timans, Jacqueline C.
;    APPLICANT:  Debets, Johannes Eduard Maria
;    APPLICANT:  Antonius
;    APPLICANT:  Sana, Theodore R.
;    APPLICANT:  Bazan, J. Fernando
;    APPLICANT:  Kastelein, Robert A.
;    TITLE OF INVENTION:  Human Receptor Proteins; Related Reagents and Methods
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/173,151A
;      FILING DATE:  14-OCT-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/065,776
;      FILING DATE:  17-NOV-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/078,008
;      FILING DATE:  12-MAR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/081,883
;      FILING DATE:  15-APR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/095,987
;      FILING DATE:  10-AUG-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/078,416
;      FILING DATE:  18-MAR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/062,066
;      FILING DATE:  15-OCT-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0767X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1200
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  482 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..480
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  9
;      OTHER INFORMATION:  /note= "residues 9, 459, 462, 469,
;      OTHER INFORMATION:  and 474 each may be A, C, G, or T; translated as C "
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  246
;      OTHER INFORMATION:  /note= "residue 246 may be C or G;
;      OTHER INFORMATION:  translated as C"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  321
;      OTHER INFORMATION:  /note= "residues 321, 335, 360, and
;      OTHER INFORMATION:  423 each may be C or T; translated as C"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  426
;      OTHER INFORMATION:  /note= "residue 426 may be A or C;
;      OTHER INFORMATION:  translated as C"
US-09-173-151A-5

Alignment Scores:
Pred. No.:                107             Length:         482
Score:                    8.00            Matches:        8
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              2.64%           Indels:         0
DB:                       4               Gaps:           0

US-10-047-021-86 (1-303) x US-09-173-151A-5 (1-482)

Qy          16 ProLeuLeuLeuLeuLeuIleMet 23
               |||||||||||||||||||||||
Db          98 CCTCTTCTGCTTCTCTTAATAATG 75

RESULT 4
US-09-621-976-264
; Sequence 264, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 264
;   LENGTH: 571
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 217..570
;   NAME/KEY: sig_peptide
;   LOCATION: 217..276
;   OTHER INFORMATION: Von Heijne matrix
;   OTHER INFORMATION: score 4.30000019073486
;   OTHER INFORMATION: seq GCLLEPFVHQVGG/HS
US-09-621-976-264

Alignment Scores:
Pred. No.:                126             Length:         571
Score:                    8.00            Matches:        8
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              2.64%           Indels:         0
DB:                       4               Gaps:           0

US-10-047-021-86 (1-303) x US-09-621-976-264 (1-571)

Qy          14 SerLeuProLeuLeuLeuLeuLeu 21
               |||||||||||||||||||||||
Db         508 TCCCTCCCTCTCCTCCTTCTCCTC 531

RESULT 5
US-08-837-029-1
; Sequence 1, Application US/08837029
; Patent No. 5945303
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  Wei et al.
;    TITLE OF INVENTION:  Human Hematopoietic - Specific Protein
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  MD
;      COUNTRY:  US
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/837,029
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US96/04930
;      FILING DATE:  11-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brookes, A. Anders
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PF268
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-309-8504
;      TELEFAX:  301-309-8439
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  833 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  42..608
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  42..107
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  108..608
US-08-837-029-1

Alignment Scores:
Pred. No.:                181             Length:         833
Score:                    8.00            Matches:        8
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              2.64%           Indels:         0
DB:                       2               Gaps:           0

US-10-047-021-86 (1-303) x US-08-837-029-1 (1-833)

Qy          14 SerLeuProLeuLeuLeuLeuLeu 21
               |||||||||||||||||||||||
Db          51 TCACTGCCACTGCTGCTGCTGCTG 74

RESULT 6
5164485-1
;Patent No. 5164485
;    APPLICANT: FUJISAWA,YUKIO; ITOH,YASUAKI; NISHIMURA,OSAMU
; FUJII,TOMOKO
;    TITLE OF INVENTION: MODIFIED HEPATITUS B VIRUS SURFACE
;ANTIGEN P31 AND PRODUCTION THEREOF
;    NUMBER OF SEQUENCES: 22
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/547,948
;      FILING DATE: 03-JUL-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 898,425
;      FILING DATE: 20-AUG-1986
;SEQ ID NO:1:
;      LENGTH: 846
5164485-1

Alignment Scores:
Pred. No.:                184             Length:         846
Score:                    8.00            Matches:        8
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              2.64%           Indels:         0
DB:                       6               Gaps:           0

US-10-047-021-86 (1-303) x 5164485-1 (1-846)

Qy          92 GlnProProAlaArgGlyHisAla 99
               |||||||||||||||||||||||
Db         506 CAACCACCAGCACGGGGCCATGCA 529

RESULT 7
US-09-615-192A-201
; Sequence 201, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
;  APPLICANT:  Bloksberg, Leonard N.
;  APPLICANT:  Havukkala, Ilkka
;  TITLE OF INVENTION:  Materials and Methods for the
;  TITLE OF INVENTION:  Modification of Plant Lignin Content
;  FILE REFERENCE:  11000.1003c4U
;  CURRENT APPLICATION NUMBER: US/09/615,192A
;  CURRENT FILING DATE:  2000-07-12
;  PRIOR APPLICATION NUMBER:  US 08/975,316
;  PRIOR FILING DATE:  1997-11-21
;  PRIOR APPLICATION NUMBER:  US 08/713,000
;  PRIOR FILING DATE:  1996-09-11
;  PRIOR APPLICATION NUMBER:  US 09/169,789
;  PRIOR FILING DATE:  1998-10-09
;  NUMBER OF SEQ ID NOS:  405
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 201
;   LENGTH: 993
;   TYPE: DNA
;   ORGANISM: Eucalyptus grandis
US-09-615-192A-201

Alignment Scores:
Pred. No.:                214             Length:         993
Score:                    8.00            Matches:        8
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              2.64%           Indels:         0
DB:                       4               Gaps:           0

US-10-047-021-86 (1-303) x US-09-615-192A-201 (1-993)

Qy          14 SerLeuProLeuLeuLeuLeuLeu 21
               |||||||||||||||||||||||
Db          53 TCCCTTCCTCTCCTCCTCCTCCTC 76

RESULT 8
US-09-976-594-522
; Sequence 522, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
```

; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 522
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 335999.1
US-09-976-594-522

Alignment Scores:

Pred. No.:	233	Length:	1081
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.64%	Indels:	0
DB:	4	Gaps:	0

US-10-047-021-86 (1-303) x US-09-976-594-522 (1-1081)

```
Qy         14 SerLeuProLeuLeuLeuLeuLeu 21
              |||||||||||||||||||||||
Db        270 TCCTTACCACTACTACTACTACTA 293
```

RESULT 9
US-10-133-907-3
; Sequence 3, Application US/10133907
; Patent No. 6677369
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII
; TITLE OF INVENTION: with vesicle vector
; FILE REFERENCE: 6627-PA1170
; CURRENT APPLICATION NUMBER: US/10/133,907
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1286
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-10-133-907-3

Alignment Scores:

Pred. No.:	275	Length:	1286
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.64%	Indels:	0
DB:	4	Gaps:	0

US-10-047-021-86 (1-303) x US-10-133-907-3 (1-1286)

```
Qy         92 GlnProProAlaArgGlyHisAla 99
              |||||||||||||||||||||||
Db        930 CAACCACCAGCACGGGGCCATGCA 953
```

RESULT 10
US-09-533-029-99
; Sequence 99, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 1339
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G515
US-09-533-029-99

Alignment Scores:

Pred. No.:	285	Length:	1339
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.64%	Indels:	0
DB:	4	Gaps:	0

US-10-047-021-86 (1-303) x US-09-533-029-99 (1-1339)

```
Qy         14 SerLeuProLeuLeuLeuLeuLeu 21
              |||||||||||||||||||||||
Db        611 AGTCTTCCTCTTCTCCTTCTTCTT 634
```

RESULT 11
US-09-668-097A-13/c
; Sequence 13, Application US/09668097A
; Patent No. 6673988
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Edgar B.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Klein, Ted
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Plant Lipases
; FILE REFERENCE: BB1401 US NA
; CURRENT APPLICATION NUMBER: US/09/668,097A
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/157309
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Glycine max
US-09-668-097A-13

Alignment Scores:

Pred. No.:	351	Length:	1662
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.64%	Indels:	0
DB:	4	Gaps:	0

US-10-047-021-86 (1-303) x US-09-668-097A-13 (1-1662)

```
Qy         15 LeuProLeuLeuLeuLeuLeuIle 22
              ||||||||||||||||||||||||
Db        664 CTACCGCTCCTTCTTCTATTAATT 641
```

```
RESULT 12
US-09-668-097A-7
; Sequence 7, Application US/09668097A
; Patent No. 6673988
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Edgar B.
;  APPLICANT:  Cahoon, Rebecca E.
;  APPLICANT:  Klein, Ted
;  APPLICANT:  Shen, Jennie
;  TITLE OF INVENTION: Plant Lipases
;  FILE REFERENCE: BB1401 US NA
;  CURRENT APPLICATION NUMBER: US/09/668,097A
;  CURRENT FILING DATE:  2000-09-22
;  PRIOR APPLICATION NUMBER: 60/157309
;  PRIOR FILING DATE: 1999-10-01
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
;   LENGTH: 1750
;   TYPE: DNA
;   ORGANISM: Oryza sativa
US-09-668-097A-7

Alignment Scores:
Pred. No.:              369             Length:         1750
Score:                  8.00            Matches:        8
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            2.64%           Indels:         0
DB:                     4               Gaps:           0

US-10-047-021-86 (1-303) x US-09-668-097A-7 (1-1750)

Qy         14 SerLeuProLeuLeuLeuLeuLeu 21
              |||||||||||||||||||||||
Db        264 TCTCTTCCTCTTCTTCTTCTTCTT 287

RESULT 13
US-08-818-112-13/c
; Sequence 13, Application US/08818112
; Patent No. 6290969
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Dillon, Davin C.
;    APPLICANT:  Campos-Neto, Antonio
;    APPLICANT:  Houghton, Raymond
;    APPLICANT:  Vedvick, Thomas S.
;    APPLICANT:  Twardzik, Daniel R.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
;    TITLE OF INVENTION:  AND DIAGNOSIS OF TUBERCULOSIS
;    NUMBER OF SEQUENCES:  153
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/818,112
;      FILING DATE:  13-MAR-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.411C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1771 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-818-112-13

Alignment Scores:
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Score:                  8.00            Matches:        8
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            2.64%           Indels:         0
DB:                     3               Gaps:           0

US-10-047-021-86 (1-303) x US-08-818-112-13 (1-1771)

Qy        234 ProValGluLeuLeuAlaValArg 241
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Db        502 CCAGTCGAACTGCTGGCTGTACGT 479

RESULT 14
US-08-818-111-13/c
; Sequence 13, Application US/08818111
; Patent No. 6338852
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Dillon, Davin C.
;    APPLICANT:  Campos-Neto, Antonia
;    APPLICANT:  Houghton, Raymond
;    APPLICANT:  Vedvick, Thomas S.
;    APPLICANT:  Twardzik, Daniel R.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR DIAGNOSIS OF    TUBERCULOSIS
;    NUMBER OF SEQUENCES:  148
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/818,111
;      FILING DATE:  13-MAR-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.417C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1771 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-818-111-13

Alignment Scores:
Pred. No.:              373             Length:         1771
Score:                  8.00            Matches:        8
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Percent Similarity: 100.00% Conservative: 0
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Query Match: 2.64% Indels: 0
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US-10-047-021-86 (1-303) x US-08-818-111-13 (1-1771)

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Db 502 CCAGTCGAACTGCTGGCTGTACGT 479

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; Sequence 13, Application US/09056556
; Patent No. 6350456
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND TREATM
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,556
; FILING DATE: 07-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.457
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-056-556-13

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.64% Indels: 0
DB: 4 Gaps: 0

US-10-047-021-86 (1-303) x US-09-056-556-13 (1-1771)

Qy 234 ProValGluLeuLeuAlaValArg 241
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Db 502 CCAGTCGAACTGCTGGCTGTACGT 479

Search completed: March 1, 2004, 07:16:08
Job time : 165 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 1, 2004, 07:16:14 ; Search time 397 Seconds
(without alignments)
2753.306 Million cell updates/sec

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Perfect score: 303
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2353733 seqs, 1803733377 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4700994

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Database : Published_Applications_NA:*
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18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	300	99.0	1346	15	US-10-047-021-31	Sequence 31, Appl
3	148	48.8	3716	9	US-09-978-295A-210	Sequence 210, App
4	148	48.8	3716	9	US-09-978-697-210	Sequence 210, App
5	148	48.8	3716	9	US-09-978-192A-210	Sequence 210, App
6	148	48.8	3716	9	US-09-999-832A-210	Sequence 210, App
7	148	48.8	3716	10	US-09-978-189-210	Sequence 210, App
8	148	48.8	3716	10	US-09-978-608A-210	Sequence 210, App
9	148	48.8	3716	10	US-09-978-585A-210	Sequence 210, App
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34	148	48.8	3716	14	US-10-017-081A-210	Sequence 210, App
35	148	48.8	3716	14	US-10-167-749-210	Sequence 210, App
36	148	48.8	3716	14	US-10-013-921A-210	Sequence 210, App
37	148	48.8	3716	14	US-10-013-929A-210	Sequence 210, App
38	148	48.8	3716	14	US-10-016-177A-210	Sequence 210, App
39	148	48.8	3716	14	US-10-166-709A-210	Sequence 210, App
40	148	48.8	3716	14	US-10-143-031A-210	Sequence 210, App
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43	148	48.8	3716	14	US-10-017-083A-210	Sequence 210, App
44	148	48.8	3716	14	US-10-145-128A-210	Sequence 210, App
45	148	48.8	3716	14	US-10-017-191A-210	Sequence 210, App

ALIGNMENTS

RESULT 1
US-10-411-224-31
; Sequence 31, Application US/10411224
; Publication No. US20030166906A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: PZ016P1
; CURRENT APPLICATION NUMBER: US/10/411,224
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/722,329
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/262,109
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 60/057,626
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,663
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/058,667
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,974
; PRIOR FILING DATE: 1997-09-12

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;  PRIOR APPLICATION NUMBER: 60/058,973
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/058,666
;  PRIOR FILING DATE: 1997-09-12
;  PRIOR APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 206
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
;   LENGTH: 1346
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (637)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (850)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-411-224-31

Alignment Scores:
Pred. No.:              8.8e-278      Length:          1346
Score:                  300.00        Matches:         303
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            99.01%        Indels:          0
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Qy         61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
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Db        271 CACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCAC 330

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Db        331 GATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 390

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Qy        241 ArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysPro 260
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Qy        261 ArgProAlaValTrpLeu***TrpLysValSerGlyPro***ArgLeuProAsnLeuThr 280
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RESULT 2
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; Publication No. US20040002591A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 50 Human Secreted Proteins
;  FILE REFERENCE: PZ016P2
;  CURRENT APPLICATION NUMBER: US/10/047,021
;  CURRENT FILING DATE:  2002-01-15
;  PRIOR APPLICATION NUMBER: US 60/262,066
;  PRIOR FILING DATE: 2001-01-18
;  PRIOR APPLICATION NUMBER: US 09/722,329
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: US 09/262,109
;  PRIOR FILING DATE: 1999-03-04
;  PRIOR APPLICATION NUMBER: PCT/US98/18360
;  PRIOR FILING DATE: 1998-09-03
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;  PRIOR APPLICATION NUMBER: US 60/090,112
;  PRIOR FILING DATE: 1998-06-22
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; SEQ ID NO 31
;   LENGTH: 1346
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
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;   OTHER INFORMATION: n equals a,t,g, or c
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US-10-047-021-31

Alignment Scores:
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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
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RESULT 3
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; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
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;  APPLICANT:  Pan, James;
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;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C11
;  CURRENT APPLICATION NUMBER: US/09/978,295A
;  CURRENT FILING DATE:  2001-10-15
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; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

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Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
Query Match:	48.84%	Indels:	4
DB:	9	Gaps:	0

US-10-047-021-86 (1-303) x US-09-978-295A-210 (1-3716)

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Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
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RESULT 4
US-09-978-697-210
; Sequence 210, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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US-10-047-021-86 (1-303) x US-09-978-697-210 (1-3716)

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Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

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;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
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;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
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;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C9
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; PRIOR APPLICATION NUMBER: 60/085697

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Best Local Similarity:	98.49%	Mismatches:	2
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DB:	9	Gaps:	0

US-10-047-021-86 (1-303) x US-09-978-192A-210 (1-3716)

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RESULT 6
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; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
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;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
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;  PRIOR APPLICATION NUMBER: 60/083499
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/083545
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/083554
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/083558
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/083559
;  PRIOR FILING DATE: 1998-04-29
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;  PRIOR FILING DATE: 1998-04-29
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;  PRIOR FILING DATE: 1998-04-30
;  PRIOR APPLICATION NUMBER: 60/084366
;  PRIOR FILING DATE: 1998-05-05
;  PRIOR APPLICATION NUMBER: 60/084414
;  PRIOR FILING DATE: 1998-05-06
;  PRIOR APPLICATION NUMBER: 60/084441
;  PRIOR FILING DATE: 1998-05-06
;  PRIOR APPLICATION NUMBER: 60/084637
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084639
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084640
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084598
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084600
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;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/085339
;  PRIOR FILING DATE: 1998-05-13
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;  PRIOR FILING DATE: 1998-05-15
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;  PRIOR FILING DATE: 1998-05-15
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;  PRIOR APPLICATION NUMBER: 60/085704
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.:              9.84e-132       Length:         3716
Score:                  148.00          Matches:        261
Percent Similarity:     98.49%          Conservative:   0
Best Local Similarity:  98.49%          Mismatches:     2
Query Match:            48.84%          Indels:         4
DB:                     9               Gaps:           0

US-10-047-021-86 (1-303) x US-09-999-832A-210 (1-3716)

Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuIleMet 23
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Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
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Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        180 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 239

Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        480 CCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539

Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        659 TTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTC 718

Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
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Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
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Db        779 CGGTGTGGCTC 789

RESULT 7
US-09-978-189-210
; Sequence 210, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
```

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-03-11
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;  PRIOR APPLICATION NUMBER: 60/084441
;  PRIOR FILING DATE: 1998-05-06
;  PRIOR APPLICATION NUMBER: 60/084637
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/084639
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;  PRIOR APPLICATION NUMBER: 60/084643
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/085339
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/085338
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/085323
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/085582
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;  PRIOR APPLICATION NUMBER: 60/085700
;  PRIOR FILING DATE: 1998-05-15
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;  PRIOR APPLICATION NUMBER: 60/085573
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;  PRIOR APPLICATION NUMBER: 60/085704
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.:                9.84e-132      Length:          3716
Score:                    148.00         Matches:         261
Percent Similarity:       98.49%         Conservative:    0
Best Local Similarity:    98.49%         Mismatches:      2
Query Match:              48.84%         Indels:          4
DB:                       10             Gaps:            0

US-10-047-021-86 (1-303) x US-09-978-189-210 (1-3716)

Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuIleMet 23
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
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Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
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Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
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Db        180 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 239

Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
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Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539

Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
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Db        659 TTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTC 718

Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
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Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
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Db        779 CGGTGTGGCTC 789

RESULT 8
US-09-978-608A-210
; Sequence 210, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C22
;  CURRENT APPLICATION NUMBER: US/09/978,608A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 210
;    LENGTH: 3716
;    TYPE: DNA
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; ORGANISM: Homo sapiens
US-09-978-608A-210

Alignment Scores:

Pred. No.:	9.84e-132	Length:	3716
Score:	148.00	Matches:	261
Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
Query Match:	48.84%	Indels:	4
DB:	10	Gaps:	0

US-10-047-021-86 (1-303) x US-09-978-608A-210 (1-3716)

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Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuIleMet 23
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
              |||||||||||||||||||||||||||||    |||||||||||||||||||||||||||
Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
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Db        180 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 239

Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
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Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
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Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
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Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
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Db        480 CCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539

Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
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Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
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Db        659 TTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTC 718

Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
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Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
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Db        779 CGGTGTGGCTC 789
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RESULT 9
US-09-978-585A-210
; Sequence 210, Application US/09978585A
; Publication No. US20030049633A1

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 210
; LENGTH: 3716
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-585A-210

Alignment Scores:

Pred. No.:	9.84e-132	Length:	3716
Score:	148.00	Matches:	261
Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
Query Match:	48.84%	Indels:	4
DB:	10	Gaps:	0

US-10-047-021-86 (1-303) x US-09-978-585A-210 (1-3716)

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Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuIleMet 23
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Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
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Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
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Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
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Db        180 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 239

Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
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Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
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Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
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Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
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Db        480 CCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539

Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
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Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
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Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
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Db        659 TTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTC 718

Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
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Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
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Db        779 CGGTGTGGCTC 789

RESULT 10
US-09-978-191A-210
; Sequence 210, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C4
;  CURRENT APPLICATION NUMBER: US/09/978,191A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/065311
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;  PRIOR APPLICATION NUMBER: 60/066364
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;  PRIOR APPLICATION NUMBER: 60/077450
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; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
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; PRIOR APPLICATION NUMBER: 60/084441
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	9.84e-132	Length:	3716
Score:	148.00	Matches:	261
Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
Query Match:	48.84%	Indels:	4
DB:	10	Gaps:	0

US-10-047-021-86 (1-303) x US-09-978-191A-210 (1-3716)

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Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuIleMet 23
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Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
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Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 239

Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
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Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
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Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
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Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539

Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
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Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
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Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
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Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
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Db        779 CGGTGTGGCTC 789

RESULT 11
US-09-978-403A-210
; Sequence 210, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C17
;  CURRENT APPLICATION NUMBER: US/09/978,403A
;  CURRENT FILING DATE:  2002-03-19
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/065311
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;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.:              9.84e-132       Length:         3716
Score:                  148.00          Matches:        261
Percent Similarity:     98.49%          Conservative:   0
Best Local Similarity:  98.49%          Mismatches:     2

Query Match:            48.84%          Indels:         4
DB:                     10              Gaps:           0

US-10-047-021-86 (1-303) x US-09-978-403A-210 (1-3716)

Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuIleMet 23
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Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
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Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

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Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
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Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
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Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
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Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
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Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
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Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
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Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
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Qy        263 laValTrpLeu 266
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RESULT 12
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; Publication No. US20030050241A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
```

; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C25
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	9.84e-132	Length:	3716
Score:	148.00	Matches:	261
Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
Query Match:	48.84%	Indels:	4
DB:	10	Gaps:	0

US-10-047-021-86 (1-303) x US-09-978-564A-210 (1-3716)

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Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuIleMet 23
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Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
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Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
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Db        180 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 239

Qy         83 uProAspGlyThrLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
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Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
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Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
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Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
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Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
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Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
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Qy        263 laValTrpLeu 266
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RESULT 13
US-09-999-833A-210
; Sequence 210, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65

; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
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;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.:                9.84e-132      Length:          3716
Score:                    148.00         Matches:         261
Percent Similarity:       98.49%         Conservative:    0
Best Local Similarity:    98.49%         Mismatches:      2
Query Match:              48.84%         Indels:          4
DB:                       10             Gaps:            0

US-10-047-021-86 (1-303) x US-09-999-833A-210 (1-3716)

Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuIleMet 23
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Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
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Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
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Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
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Db        180 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 239

Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
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Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

Qy        123 aValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGlnIleGlnPr 143
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Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
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Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539

Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
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Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
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Db        659 TTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTC 718

Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
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Db        779 CGGTGTGGCTC 789
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RESULT 14
US-09-981-915A-210
; Sequence 210, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C12
;  CURRENT APPLICATION NUMBER: US/09/981,915A
;  CURRENT FILING DATE:  2001-10-16
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
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;  PRIOR FILING DATE: 1998-03-12
;  PRIOR APPLICATION NUMBER: 60/078004
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; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
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; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

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Pred. No.:              9.84e-132       Length:         3716
Score:                  148.00          Matches:        261
Percent Similarity:     98.49%          Conservative:   0
Best Local Similarity:  98.49%          Mismatches:     2
Query Match:            48.84%          Indels:         4
DB:                     10              Gaps:           0

US-10-047-021-86 (1-303) x US-09-981-915A-210 (1-3716)

Qy          4 GlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeuLeuIleMet 23
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Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
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Db        121 CAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACCTCCCACCAT 179

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACACCACCTCCT 239

Qy         83 uProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHisAspGlyGl 103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCA 299

Qy        103 nAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeuGlyThrAl 123
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Db        300 GGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGC 359

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Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

Qy        143 oArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyProProTrpGl 163
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Db        420 TCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCGCCCTGGGG 479

Qy        163 yHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeuGlnProGl 183
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Db        480 CCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTCCAGCCCGG 539

Qy        183 yArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSerAspGlu** 203
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Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
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Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

Qy        223 alSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaValArgIleG 243
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Db        659 TTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTC 718

Qy        243 lnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysProArgProA 263
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Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
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Db        779 CGGTGTGGCTC 789

RESULT 15
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; Sequence 210, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C14
;  CURRENT APPLICATION NUMBER: US/09/978,824
;  CURRENT FILING DATE:  2001-10-17
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:

Pred. No.:	9.84e-132	Length:	3716
Score:	148.00	Matches:	261
Percent Similarity:	98.49%	Conservative:	0
Best Local Similarity:	98.49%	Mismatches:	2
Query Match:	48.84%	Indels:	4
DB:	10	Gaps:	0

US-10-047-021-86 (1-303) x US-09-978-824-210 (1-3716)

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATG 60

Qy         24 GlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAspGlnLeuPhe 43
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Db         61 GGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTC 120

Qy         44 GlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProProProThrIl 63
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Qy         63 eArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHisHisLeuLe 83
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Db        360 AGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCC 419

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Db        540 AAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGG 599

Qy        203 *-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgAlaAlaArgV 223
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Db        600 -GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGG 658

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Db        719 AGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGCCTAGACCGG 778

Qy        263 laValTrpLeu 266
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Db        779 CGGTGTGGCTC 789
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Search completed: March 1, 2004, 10:25:57
Job time : 413 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 29, 2004, 08:16:48 ; Search time 27 Seconds
(without alignments)
1079.483 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 303
Sequence: 1 MGSGGDSLLGGRGSLPLLLL.....SGPRLPREARELRGQRRNTG 303

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10	3.3	1209	2	T42718	probable neural ce
2	8	2.6	72	2	AD3406	hypothetical membr
3	8	2.6	233	2	G86703	oxidoreductase ygc
4	8	2.6	431	2	T04868	hypothetical prote
5	8	2.6	437	2	S59151	NADH2 dehydrogenas
6	8	2.6	444	2	G97431	hypothetical prote
7	8	2.6	453	2	AH2649	conserved hypothet
8	8	2.6	991	2	I49540	procollagen C-endo
9	8	2.6	1102	2	JH0717	guanylate cyclase
10	8	2.6	1501	2	I58148	protein-tyrosine-p
11	8	2.6	1863	2	S46217	protein-tyrosine-p
12	8	2.6	1894	2	C54689	protein-tyrosine-p
13	8	2.6	1897	1	TDHULK	leukocyte antigen-
14	8	2.6	1898	2	S46216	leukocyte antigen-
15	8	2.6	1907	2	S50893	protein-tyrosine-p
16	8	2.6	1912	2	A56178	protein-tyrosine-p
17	8	2.6	6642	2	T29757	protein UNC-89 - C
18	7	2.3	18	2	I52614	u-plasminogen acti
19	7	2.3	24	2	I67553	monocyte chemotact
20	7	2.3	30	2	G45087	cysteine proteinas
21	7	2.3	51	2	S64676	acetylcholinestera
22	7	2.3	92	2	C75348	hypothetical prote
23	7	2.3	96	2	S33145	NADH2 dehydrogenas
24	7	2.3	100	2	S14490	Ig heavy chain V r
25	7	2.3	100	2	A38685	apolipoprotein C-I
26	7	2.3	106	2	S14489	Ig heavy chain V r
27	7	2.3	106	2	T06479	proline/leucine-ri
28	7	2.3	107	2	S14492	Ig heavy chain V r
29	7	2.3	107	2	S14493	Ig heavy chain V r
30	7	2.3	117	2	S25176	Ig heavy chain V r
31	7	2.3	118	2	S24443	Ig heavy chain V r
32	7	2.3	120	2	F71126	hypothetical prote
33	7	2.3	122	2	T49667	hypothetical prote
34	7	2.3	134	2	S70811	hypothetical prote
35	7	2.3	136	2	T25840	hypothetical prote
36	7	2.3	140	2	AF3282	hypothetical prote
37	7	2.3	147	2	JC7237	receptor-activity-
38	7	2.3	147	2	JC7263	receptor activity
39	7	2.3	166	2	T07089	dehydrin - soybean
40	7	2.3	184	2	S10125	alpha-2u-globulin
41	7	2.3	193	2	AF1323	3-isopropylmalate
42	7	2.3	193	2	AG1694	3-isopropylmalate
43	7	2.3	193	2	S35613	ganglioside M2 act
44	7	2.3	209	2	A54984	ELF-1 protein prec
45	7	2.3	213	2	JE0322	ephrin-A2 - human

ALIGNMENTS

RESULT 1
T42718
probable neural cell adhesion molecule L1 precursor - mouse
N;Alternate names: CHL1 protein
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 20-Jun-2000
C;Accession: T42718
R;Holm, J.; Hillenbrand, R.; Steuber, V.; Bartsch, U.; Moos, M.; Luebbert, H.; Montag, D
submitted to the EMBL Data Library, December 1995
A;Description: Structural features of a close homolog of L1 (CHL1) in the mouse: a novel
A;Reference number: Z22239
A;Accession: T42718
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1209 <HOL>
A;Cross-references: EMBL:X94310; PIDN:CAA63972.1
A;Experimental source: brain
C;Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; in
C;Keywords: cell adhesion; duplication; glycoprotein; transmembrane protein

Query Match 3.3%; Score 10; DB 2; Length 1209;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        116 ASNRLGTAVS 125
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Db        111 ASNRLGTAVS 120
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RESULT 2
AD3406
hypothetical membrane associated protein BMEI1234 [imported] - Brucella melitensis (stra
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AD3406
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesso
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AD3406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-72 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52415.1; PID:g17983217; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1234
A;Map position: I

Query Match 2.6%; Score 8; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          13 GSLPLLLL 20
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Db          44 GSLPLLLL 51
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RESULT 3
G86703
oxidoreductase ygcA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: G86703
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G86703
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <STO>
A;Cross-references: GB:AE005176; PID:g12723534; PIDN:AAK04729.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ygcA

Query Match 2.6%; Score 8; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         243 QLENVTLL 250
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Db          45 QLENVTLL 52
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RESULT 4
T04868
hypothetical protein F28A21.170 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C;Accession: T04868
R;Bevan, M.; Mueller, M.W.; Muendlein, A.; Felber, R.; Bancroft, I.; Mewes, H.W.; Mayer,
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15387
A;Accession: T04868
A;Molecule type: DNA
A;Residues: 1-431 <BEV>
A;Cross-references: EMBL:AL035526
A;Experimental source: cultivar Columbia; BAC clone F28A21
C;Genetics:
A;Map position: 4
A;Note: F28A21.170

Query Match 2.6%; Score 8; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          14 SLPLLLLL 21
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Db           5 SLPLLLLL 12
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RESULT 5
S59151
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - land snail mitochondrion
C;Species: mitochondrion Albinaria coerulea (land snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
C;Accession: S59151
R;Hatzoglou, E.; Rodakis, G.C.; Lecanidou, R.
Genetics 140, 1353-1366, 1995
A;Title: Complete sequence and gene organization of the mitochondrial genome of the land
A;Reference number: S59143; MUID:96120351; PMID:7498775
A;Accession: S59151
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-437 <HAT>
A;Cross-references: EMBL:X83390; NID:g975668; PIDN:CAA58304.1; PID:g975677; GSPDB:GN00133
C;Genetics:
A;Gene: ND4
A;Genome: mitochondrion
A;Genetic code: SGC4
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c

Query Match 2.6%; Score 8; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          14 SLPLLLLL 21
               ||||||||
Db         142 SLPLLLLL 149
```

RESULT 6
G97431
hypothetical protein AGR_C_1055 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: G97431
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G97431
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-444 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86408.1; PID:g15155542; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_1055
A;Map position: circular chromosome

Query Match 2.6%; Score 8; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          82 LLPDGTLL 89
               ||||||||
Db         214 LLPDGTLL 221
```

RESULT 7
AH2649
conserved hypothetical protein Atu0597 [imported] - Agrobacterium tumefaciens (strain C58
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AH2649
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClella
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, B
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH2649
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-453 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41614.1; PID:g17738952; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu0597
A;Map position: circular chromosome

Query Match 2.6%; Score 8; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 LLPDGTLL 89
||||||||
Db 223 LLPDGTLL 230

RESULT 8
I49540
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I49540
R;Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.
Dev. Biol. 163, 175-183, 1994
A;Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rel
A;Reference number: I49540; MUID:94229342; PMID:8174772
A;Accession: I49540
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-991 <RES>
A;Cross-references: GB:L24755; NID:g439606; PIDN:AAA37306.1; PID:g439607
C;Genetics:
A;Gene: Bmp-1
C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
C;Keywords: hydrolase; metalloproteinase; zinc
F;135-326/Domain: astacin homology <AST>
F;556-592/Domain: EGF homology <EG1>
F;596-705/Domain: C1r/C1s repeat homology <C1R>
F;712-747/Domain: EGF homology <EG2>
F;218,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted
F;219/Active site: Glu #status predicted

Query Match 2.6%; Score 8; DB 2; Length 991;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 SLPLLLLL 21
||||||||
Db 13 SLPLLLLL 20

RESULT 9
JH0717
guanylate cyclase (EC 4.6.1.2) 2D precursor, retinal - human
N;Alternate names: guanylyl cyclase; retinal guanylate cyclase 1
C;Species: Homo sapiens (man)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 16-Jul-1999
C;Accession: JH0717; A55186
R;Shyjan, A.W.; de Sauvage, F.J.; Gillett, N.A.; Goeddel, D.V.; Lowe, D.G.
Neuron 9, 727-737, 1992
A;Title: Molecular cloning of a retina-specific membrane guanylyl cyclase.
A;Reference number: JH0717; MUID:93001163; PMID:1356371
A;Accession: JH0717
A;Molecule type: mRNA
A;Residues: 1-1102 <SHY>
A;Cross-references: GB:M92432
A;Experimental source: retina
R;Oliveira, L.; Miniou, P.; Viegas-Pequignot, E.; Rozet, J.M.; Dollfus, H.; Pittler, S.J
Genomics 22, 478-481, 1994
A;Title: Human retinal guanylate cyclase (GUC2D) maps to chromosome 17p13.1.
A;Reference number: A55186; MUID:95104866; PMID:7806240
A;Accession: A55186
A;Molecule type: DNA
A;Residues: 1001-1087 <OLI>
A;Cross-references: GB:L26921
C;Genetics:
A;Gene: GDB:GUC2D
A;Cross-references: GDB:136012; OMIM:600179
A;Map position: 17p13-17p13
C;Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain homd
C;Keywords: cGMP biosynthesis; glycoprotein; phosphorus-oxygen lyase; transmembrane prote
F;1-51/Domain: signal sequence #status predicted <SIG>
F;52-1102/Product: guanylate cyclase #status predicted <MAT>
F;463-487/Domain: transmembrane #status predicted <TMM>
F;524-811/Domain: protein kinase homology <KIN>
F;831-1059/Domain: guanylate cyclase catalytic domain homology <GCC>

Query Match 2.6%; Score 8; DB 2; Length 1102;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 88 LLLLQPPA 95
||||||||
Db 42 LLLLQPPA 49

RESULT 10
I58148
protein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form LAR - rat
N;Alternate names: leukocyte common antigen-related phosphatase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000
C;Accession: I58148; S46218
R;Walton, K.M.; Martell, K.J.; Kwak, S.P.; Dixon, J.E.; Largent, B.L.
Neuron 11, 387-400, 1993
A;Title: A novel receptor-type protein tyrosine phosphatase is expressed during neurogene
A;Reference number: I58148; MUID:93357030; PMID:8352946
A;Accession: I58148
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1501 <WAL>
A;Cross-references: GB:L19933; NID:g310242; PIDN:AAA42309.1; PID:g310243
A;Note: in Genbank entry RATTYRPHOS, release 113.0, the source is designated as Rattus ra
R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem. J. 302, 39-47, 1994
A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phos
A;Reference number: S46216; MUID:94347119; PMID:8068021
A;Accession: S46218
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-1501 <ZHA>
A;Cross-references: EMBL:L12329; NID:g294573; PIDN:AAC37657.1; PID:g294574
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy
C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosi
F;47-109/Domain: immunoglobulin homology <IMM1>
F;149-209/Domain: immunoglobulin homology <IMM2>
F;246-300/Domain: immunoglobulin homology <IMM3>
F;413-506/Domain: fibronectin type III repeat homology <3FR>
F;882-1501/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;969-1190/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1258-1481/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1142/Active site: Cys (phosphocysteine intermediate) #link PTP1 #status predicted
F;1148/Binding site: substrate phosphate (Arg) #link PTP1 #status predicted
F;1433/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted
F;1439/Binding site: substrate phosphate (Arg) #link PTP2 #status predicted

Query Match 2.6%; Score 8; DB 2; Length 1501;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 CVATNSAG 214
||||||||
Db 207 CVATNSAG 214

RESULT 11
S46217
protein-tyrosine-phosphatase (EC 3.1.3.48) type sigma precursor - rat
N;Alternate names: leukocyte common antigen-related phosphatase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S46217; S51174; A49104

R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem. J. 302, 39-47, 1994
A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phc
A;Reference number: S46216; MUID:94347119; PMID:8068021
A;Accession: S46217
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1863 <ZHA>
A;Cross-references: EMBL:L11587
R;Goldstein, B.J.
submitted to the EMBL Data Library, February 1993
A;Reference number: S51174
A;Accession: S51174
A;Molecule type: mRNA
A;Residues: 1-1788,'G',1790-1863 <GOL>
A;Cross-references: EMBL:L11587; NID:g205134; PIDN:AAC37656.1; PID:g205135
R;Yan, H.; Grossman, A.; Wang, H.; D'Eustachio, P.; Mossie, K.; Musacchio, J.M.; Silvenn
J. Biol. Chem. 268, 24880-24886, 1993
A;Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the ner
A;Reference number: A49104; MUID:94043351; PMID:8227050
A;Accession: A49104
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-596,'R',598-603,'I',967-1788,'G',1790-1863 <YAN>
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:139669)
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy
C;Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-1863/Product: protein-tyrosine-phosphatase #status predicted <MAT>
F;149-209/Domain: immunoglobulin homology <IMM1>
F;246-300/Domain: immunoglobulin homology <IMM2>
F;318-400/Domain: fibronectin type III repeat homology <FN3A>
F;413-499/Domain: fibronectin type III repeat homology <FN3B>
F;511-592/Domain: fibronectin type III repeat homology <FN3C>
F;1244-1863/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1331-1552/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1504/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1510/Binding site: substrate phosphate (Arg) #status predicted
F;1795/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1801/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.6%; Score 8; DB 2; Length 1863;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 CVATNSAG 214
||||||||
Db 207 CVATNSAG 214

RESULT 12
C54689
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor
N;Alternate names: MPTP delta type B/C
N;Contains: protein tyrosine phosphatase, receptor type delta, splice form C
C;Species: Mus musculus (house mouse)
C;Date: 25-Apr-1995 #sequence_revision 19-May-1995 #text_change 12-Feb-1999
C;Accession: C54689; B54689
R;Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
Mol. Cell. Biol. 13, 5513-5523, 1993
A;Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialize
A;Reference number: A54689; MUID:93360986; PMID:8355697
A;Accession: C54689
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1894 <MIZ>
A;Experimental source: brain; splice form B
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIP:137487)
A;Accession: B54689
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-352,'H',354-535,'S',537-601,1002-1894 <MI2>
A;Experimental source: brain; splice form C
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBIP:136530)
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; i
ogy
C;Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
F;45-107/Domain: immunoglobulin homology <IMM1>
F;245-299/Domain: immunoglobulin homology <IMM2>
F;317-399/Domain: fibronectin type III repeat homology <FN3A>
F;1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1536/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1542/Binding site: substrate phosphate (Arg) #status predicted
F;1826/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1832/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.6%; Score 8; DB 2; Length 1894;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 CVATNSAG 214
||||||||
Db 208 CVATNSAG 215

RESULT 13
TDHULK
leukocyte antigen-related protein precursor - human
N;Alternate names: leukocyte common antigen homolog
N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
C;Accession: S03841; JL0051
R;Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.
J. Exp. Med. 168, 1523-1530, 1988
A;Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region hon
A;Reference number: JL0051; MUID:89035978; PMID:2972792
A;Accession: S03841
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1897 <STR>
A;Cross-references: EMBL:Y00815; NID:g34266; PIDN:CAA68754.1; PID:g34267
C;Genetics:
A;Gene: GDB:PTPRF; LAR
A;Cross-references: GDB:120138; OMIM:179590
A;Map position: 1p34-1p34
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; i
ogy
C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane p
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>
F;17-1250/Domain: extracellular #status predicted <EXT>
F;37-99/Domain: immunoglobulin homology <IMM1>
F;139-199/Domain: immunoglobulin homology <IMM2>
F;236-290/Domain: immunoglobulin homology <IMM3>
F;308-390/Domain: fibronectin type III repeat homology <FN3A>
F;403-489/Domain: fibronectin type III repeat homology <FN3B>
F;501-583/Domain: fibronectin type III repeat homology <FN3C>
F;596-685/Domain: fibronectin type III repeat homology <FN3D>
F;698-798/Domain: fibronectin type III repeat homology #status atypical <FN3E>
F;810-893/Domain: fibronectin type III repeat homology <FN3F>
F;905-989/Domain: fibronectin type III repeat homology <FN3G>
F;1001-1078/Domain: fibronectin type III repeat homology <FN3H>
F;1251-1274/Domain: transmembrane #status predicted <TMM>
F;1275-1897/Domain: intracellular #status predicted <INT>
F;1285-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1365-1586/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;44-97,146-197,243-288/Disulfide bonds: #status predicted
F;107,240,285,711,956/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1538/Active site: Cys (phosphocysteine intermediate) #status predicted

F;1544/Binding site: substrate phosphate (Arg) #status predicted
F;1829/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1835/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.6%; Score 8; DB 1; Length 1897;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 CVATNSAG 214
||||||||
Db 197 CVATNSAG 204

RESULT 14
S46216
leukocyte antigen-related protein precursor - rat
N;Alternate names: leukocyte common antigen homolog
N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S46216; S23252; A41032; A33154
R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem. J. 302, 39-47, 1994
A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-pho
A;Reference number: S46216; MUID:94347119; PMID:8068021
A;Accession: S46216
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1898 <ZHA>
A;Cross-references: EMBL:L11586; NID:g205132; PIDN:AAC37655.1; PID:g205133
R;Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.
Biochem. J. 284, 569-576, 1992
A;Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by thre
A;Reference number: S23126; MUID:92287069; PMID:1599438
A;Accession: S23252
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1361-1604;1649-1898 <HAS>
R;Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
J. Biol. Chem. 266, 19688-19696, 1991
A;Title: Cloning, bacterial expression, purification, and characterization of the cytopl
A;Reference number: A41032; MUID:92011772; PMID:1918076
A;Accession: A41032
A;Molecule type: mRNA
A;Residues: 1035-1072,'S',1074-1433,'T',1435-1638,'N',1640-1642,'HT',1645-1898 <POT>
A;Cross-references: GB:M60103; NID:g205130; PIDN:AAA41510.1; PID:g205131
R;Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.
submitted to the Protein Sequence Database, December 1990
A;Reference number: A33154
A;Accession: A33154
A;Molecule type: mRNA
A;Residues: 1035-1072,'S',1074-1433,'T',1435-1638,'N',1640-1642,'HT',1645-1898 <PO2>
C;Comment: Only the first of the two domains homologous with protein-tyrosine-phosphatas
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy
C;Keywords: duplication; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; t
F;1-27/Domain: (or 1-26) signal sequence #status predicted <SIG>
F;28-1898/Product: (or 27-1898) leukocyte antigen-related protein #status predicted <MAT
F;28-1251/Domain: (or 27-1251) extracellular #status predicted <EXT>
F;47-109/Domain: immunoglobulin homology <IMM1>
F;149-209/Domain: immunoglobulin homology <IMM2>
F;246-300/Domain: immunoglobulin homology <IMM3>
F;318-400/Domain: fibronectin type III repeat homology <FN3A>
F;413-499/Domain: fibronectin type III repeat homology <FN3B>
F;511-593/Domain: fibronectin type III repeat homology <FN3C>
F;606-695/Domain: fibronectin type III repeat homology <FN3D>
F;708-799/Domain: fibronectin type III repeat homology <FN3E>
F;811-895/Domain: fibronectin type III repeat homology <FN3F>
F;906-990/Domain: fibronectin type III repeat homology <FN3G>
F;1002-1079/Domain: fibronectin type III repeat homology <FN3H>
F;1252-1275/Domain: (or 1259-1275) transmembrane #status predicted <TMM>
F;1276-1898/Domain: intracellular #status predicted <INT>
F;1286-1898/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1366-1587/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1655-1878/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;54-107,156-207,253-298/Disulfide bonds: #status predicted
F;117,250,295,721,957/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1539/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1545/Binding site: substrate phosphate (Arg) #status predicted
F;1830/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1836/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.6%; Score 8; DB 2; Length 1898;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 CVATNSAG 214
||||||||
Db 207 CVATNSAG 214

RESULT 15
S50893
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S50893; S40281
R;Wagner, J.; Boerboom, D.; Tremblay, M.L.
Eur. J. Biochem. 226, 773-782, 1994
A;Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-type p
A;Reference number: S50893; MUID:95112841; PMID:7529177
A;Accession: S50893
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1907 <WAG>
A;Cross-references: EMBL:X82288; NID:g587483; PIDN:CAA57732.1; PID:g587484
R;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A;Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
A;Reference number: S40280
A;Accession: S40281
A;Molecule type: mRNA
A;Residues: 1441-1501,'E',1503-1546 <HEN>
A;Cross-references: EMBL:Z23050; NID:g438137; PIDN:CAA80585.1; PID:g438138
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; i
ogy
C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane p
F;149-209/Domain: immunoglobulin homology <IMM1>
F;246-300/Domain: immunoglobulin homology <IMM2>
F;413-506/Domain: fibronectin type III repeat homology <3FR>
F;1288-1907/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1375-1596/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1664-1887/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1548/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1554/Binding site: substrate phosphate (Arg) #status predicted
F;1839/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1845/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.6%; Score 8; DB 2; Length 1907;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 CVATNSAG 214
||||||||
Db 207 CVATNSAG 214

Search completed: February 29, 2004, 08:17:50
Job time : 32 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 27, 2004, 17:38:30 ; Search time 19 Seconds
(without alignments)
830.382 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 303
Sequence: 1 MGSGGDSLLGGRGSLPLLLL.....SGPRLPREARELRGQRRNTG 303

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8	2.6	120	1	SY27_MOUSE	Q9z1x0 mus musculu
2	8	2.6	205	1	RNS9_CEBAL	Q7yrg8 cebus albif
3	8	2.6	437	1	NU4M_ALBCO	P48914 albinaria c
4	8	2.6	469	1	MM01_HORSE	Q9xsz5 equus cabal
5	8	2.6	991	1	BMP1_MOUSE	P98063 mus musculu
6	8	2.6	1103	1	CYGD_HUMAN	Q02846 homo sapien
7	8	2.6	1897	1	PTPF_HUMAN	P10586 homo sapien
8	8	2.6	1912	1	PTPD_HUMAN	P23468 homo sapien
9	8	2.6	1948	1	PTNS_HUMAN	Q13332 homo sapien
10	8	2.6	6632	1	UN89_CAEEL	O01761 caenorhabdi
11	7	2.3	96	1	NU6M_ALBTU	Q08084 albinaria t
12	7	2.3	100	1	APC2_CAVPO	P27916 cavia porce
13	7	2.3	112	1	SZ06_BOVIN	P80221 bos taurus
14	7	2.3	147	1	RMP3_MOUSE	Q9wup1 mus musculu
15	7	2.3	148	1	RMP3_HUMAN	O60896 homo sapien
16	7	2.3	153	1	RNS6_MOUSE	Q9d244 mus musculu
17	7	2.3	164	1	UCN3_MOUSE	Q924a4 mus musculu
18	7	2.3	184	1	MUP3_MOUSE	P04939 mus musculu
19	7	2.3	184	1	RNS9_MOUSE	P60154 mus musculu
20	7	2.3	185	1	NPW_RAT	Q8klm5 rattus norv
21	7	2.3	193	1	LEUD_LISIN	Q92a25 listeria in
22	7	2.3	193	1	LEUD_LISMO	Q8y5r6 listeria mo
23	7	2.3	193	1	SAP3_MOUSE	Q60648 mus musculu
24	7	2.3	202	1	COAE_XANAC	Q8phk7 xanthomonas
25	7	2.3	204	1	RNS9_HYLSY	Q863j9 hylobates s
26	7	2.3	204	1	RNS9_PONPY	Q7yrh4 pongo pygma
27	7	2.3	205	1	BEL1_FOAMV	P14353 human spuma
28	7	2.3	205	1	RNS9_GORGO	Q863k0 gorilla gor
29	7	2.3	207	1	COAE_XANCP	Q56764 xanthomonas
30	7	2.3	209	1	EFA2_MOUSE	P52801 mus musculu
31	7	2.3	212	1	NOG2_BRARE	Q9w740 brachydanio
32	7	2.3	213	1	EFA2_HUMAN	O43921 homo sapien
33	7	2.3	225	1	CBS1_ARCFU	O30198 archaeoglob
34	7	2.3	238	1	GIDB_LACLA	Q9cfx1 lactococcus
35	7	2.3	242	1	EPCR_MOUSE	Q64695 mus musculu
36	7	2.3	245	1	CG21_MOUSE	Q9jmg3 mus musculu
37	7	2.3	246	1	CG21_HUMAN	Q9bvt8 homo sapien
38	7	2.3	248	1	MABC_HUMAN	P11226 homo sapien
39	7	2.3	249	1	YBG0_STRCO	P40179 streptomyce
40	7	2.3	255	1	MFA4_HUMAN	P55083 homo sapien
41	7	2.3	267	1	PIV6_ADE40	P48309 human adeno
42	7	2.3	281	1	POTI_ECOLI	P31136 escherichia
43	7	2.3	318	1	NSR_LACLA	P23648 lactococcus
44	7	2.3	328	1	IBP2_HUMAN	P18065 homo sapien
45	7	2.3	330	1	YBJX_ECOLI	P75829 escherichia

ALIGNMENTS

RESULT 1
SY27_MOUSE
ID SY27_MOUSE STANDARD; PRT; 120 AA.
AC Q9Z1X0; Q9DAU6; Q9DAZ4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A27 precursor (CCL27) (CC chemokine ILC) (IL-
DE 11 Ralpha-locus chemokine) (mILC) (ALP) (Skinkine) (ESkine)
DE (Cuteaneous T-cell attracting chemokine) (CTACK).
GN CCL27 OR SCYA27 OR ILC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99262167; PubMed=10329455;
RA Hromas R., Broxmeyer H.E., Kim C., Christopherson K. II, Hou Y.-H.;
RT "Isolation of ALP, a novel divergent murine CC chemokine with a unique
RT carboxy terminal extension.";
RL Biochem. Biophys. Res. Commun. 258:737-740(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20026096; PubMed=10556532;
RA Ishikawa-Mochizuki I., Kitaura M., Baba M., Nakayama T., Izawa D.,
RA Imai T., Yamada H., Hieshima K., Suzuki R., Nomiyama H., Yoshie O.;
RT "Molecular cloning of a novel CC chemokine, interleukin-11 receptor
RT alpha-locus chemokine (ILC), which is located on chromosome 9p13 and a
RT potential homologue of a CC chemokine encoded by molluscum contagiosum
RT virus.";
RL FEBS Lett. 460:544-548(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20056268; PubMed=10588729;
RA Morales J., Homey B., Vicari A.P., Hudak S., Oldham E., Hedrick J.,
RA Orozco R., Copeland N.G., Jenkins N.A., McEvoy L.M., Zlotnik A.;
RT "CTACK, a skin-associated chemokine that preferentially attracts
RT skin-homing memory T cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:14470-14475(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

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RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   SUBCELLULAR LOCATION, AND ALTERNATIVE SPLICING.
RC   TISSUE=Placenta, and Testis;
RX   MEDLINE=20026881; PubMed=10559234;
RA   Baird J.W., Nibbs R.J.B., Komai-Koma M., Connolly J.A., Ottersbach K.,
RA   Clark-Lewis I., Liew F.Y., Graham G.J.;
RT   "ESkine, a novel beta-chemokine, is differentially spliced to produce
RT   secretable and nuclear targeted isoforms.";
RL   J. Biol. Chem. 274:33496-33503(1999).
RN   [7]
RP   SUBCELLULAR LOCATION.
RX   MEDLINE=22129044; PubMed=12133963;
RA   Gortz A., Nibbs R.J.B., McLean P., Jarmin D., Lambie W., Baird J.W.,
RA   Graham G.J.;
RT   "The chemokine ESkine/CCL27 displays novel modes of intracrine and
RT   paracrine function.";
RL   J. Immunol. 169:1387-1394(2002).
CC   -!- FUNCTION: Chemotactic factor that attracts skin-associated memory
CC       T-lymphocytes. May play a role in mediating homing of lymphocytes
CC       to cutaneous sites. May play a role in cell migration during
CC       embryogenesis. Nuclear forms may facilitate cellular migration by
CC       inducing cytoskeletal relaxation. Binds to CCR10.
CC   -!- SUBCELLULAR LOCATION: Secreted (isoform 1) or nuclear (isoform 2).
CC       Isoform 1 may also be nuclear when following receptor (CCR10)-
CC       mediated internalization.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q9Z1X0-1; Sequence=Displayed;
CC       Name=2; Synonyms=PESKY;
CC         IsoId=Q9Z1X0-2; Sequence=VSP_001065;
CC   -!- TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in
CC       placenta and weakly in skin. Isoform 2 is predominantly expressed
CC       in testes and brain, weakly in kidney and liver and even lower in
CC       heart and muscle. Low expression of both isoforms in other
CC       tissues.
CC   -!- DEVELOPMENTAL STAGE: Expressed during development.
CC   -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC   -!- CAUTION: It is uncertain whether Met-1 or Met-2 is the initiator.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF099931; AAD04163.1; -.
DR   EMBL; AB013398; BAA88474.1; -.
DR   EMBL; AF082392; AAD41237.1; -.
DR   EMBL; AK005520; BAB24095.1; -.
DR   EMBL; AK005398; BAB24001.1; -.
DR   EMBL; BC028511; AAH28511.1; -.
DR   MGD; MGI:1343459; Ccl27.
DR   GO; GO:0005125; F:cytokine activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR000827; CC_chemkine_sml.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00472; SMALL_CYTOKINES_CC; FALSE_NEG.
KW   Cytokine; Nuclear protein; Signal; Alternative splicing.
FT   SIGNAL       1     25       POTENTIAL.
FT   CHAIN       26    120       SMALL INDUCIBLE CYTOKINE A27.
FT   DISULFID    34     63       BY SIMILARITY.
FT   DISULFID    35     78       BY SIMILARITY.
FT   VARSPLIC     1     24       MMEGLSPASSLPLLLLLLSPAPEA -> MWRRERSPMSPTS
FT                                QRLSLEAPSLPLRSWHPWNKTKQKQE (in isoform
FT                                2).
FT                                /FTId=VSP_001065.
FT   CONFLICT   115    115       H -> N (IN REF. 1, 2 AND 3).
SQ   SEQUENCE   120 AA;  13464 MW;  D1EEE1270AB580BF CRC64;

  Query Match             2.6%;  Score 8;  DB 1;  Length 120;
  Best Local Similarity   100.0%;  Pred. No. 2.9;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 SLPLLLLL 21
              ||||||||
Db         10 SLPLLLLL 17


RESULT 2
RNS9_CEBAL
ID   RNS9_CEBAL     STANDARD;      PRT;   205 AA.
AC   Q7YRG8;
DT   15-MAR-2004 (Rel. 43, Created)
DT   15-MAR-2004 (Rel. 43, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ribonuclease-like protein 9 precursor.
GN   RNASE9.
OS   Cebus albifrons (White-fronted capuchin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
OX   NCBI_TaxID=9514;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Devor E.J., Moffat-Wilson K.A.;
RT   "LOC122650 on chromosome 14q11.2 is related to the RNase A superfamily
RT   and contains a unique amino-terminal pre-protein-like domain.";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY330198; AAQ01508.1; -.
DR   InterPro; IPR001427; RNaseA.
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DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
KW   Signal.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    205       RIBONUCLEASE-LIKE PROTEIN 9.
FT   DISULFID     97    152       BY SIMILARITY.
FT   DISULFID    115    167       BY SIMILARITY.
FT   DISULFID    122    129       BY SIMILARITY.
FT   CARBOHYD    130    130       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    142    142       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   205 AA;  24294 MW;  DBFC3217F7A070D0 CRC64;

  Query Match             2.6%;  Score 8;  DB 1;  Length 205;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 SLPLLLLL 21
              ||||||||
Db          8 SLPLLLLL 15


RESULT 3
NU4M_ALBCO
ID   NU4M_ALBCO     STANDARD;      PRT;   437 AA.
AC   P48914;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-FEB-1996 (Rel. 33, Last annotation update)
DE   NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
GN   ND4.
OS   Albinaria coerulea (Land snail).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC   Sigmurethra; Clausilioidea; Clausiliidae; Alopiinae; Albinaria.
OX   NCBI_TaxID=42349;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96120351; PubMed=7498775;
RA   Hatzoglou E., Rodakis G.C., Lecanidou R.;
RT   "Complete sequence and gene organization of the mitochondrial genome
RT   of the land snail Albinaria coerulea.";
RL   Genetics 140:1353-1366(1995).
CC   -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X83390; CAA58304.1; -.
DR   PIR; S59151; S59151.
DR   InterPro; IPR003918; NADHub_oxred4.
DR   InterPro; IPR001750; Oxidored_q1.
DR   Pfam; PF00361; oxidored_q1; 1.
DR   PRINTS; PR01437; NUOXDRDTASE4.
KW   Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ   SEQUENCE   437 AA;  49159 MW;  2A63927F187CA4D0 CRC64;

  Query Match             2.6%;  Score 8;  DB 1;  Length 437;
  Best Local Similarity   100.0%;  Pred. No. 9.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 SLPLLLLL 21
              ||||||||
Db        142 SLPLLLLL 149


RESULT 4
MM01_HORSE
ID   MM01_HORSE     STANDARD;      PRT;   469 AA.
AC   Q9XSZ5;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE   metalloproteinase-1) (MMP-1).
GN   MMP1.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Richardson D.W.;
RT   "Cloning and expression of equine matrix metalloproteinase 1
RT   (interstitial collagenase).";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC       the helical domain. Also cleaves collagens of types VII and X.
CC   -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC       collagen. Cleavage of the triple helix of collagen at about three-
CC       quarters of the length of the molecule from the N-terminus, at
CC       775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC       substrates and alpha-macroglobulins at bonds where P1' is a
CC       hydrophobic residue.
CC   -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC       similarity).
CC   -!- ENZYME REGULATION: Can be activated without removal of the
CC       activation peptide.
CC   -!- SIMILARITY: Belongs to peptidase family M10A.
CC   -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF148882; AAD38030.1; -.
DR   HSSP; P03956; 1AYK.
DR   MEROPS; M10.001; -.
DR   InterPro; IPR000585; Hemopexin.
DR   InterPro; IPR001818; Pept_M10A_M12B.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR006026; Peptidase_M.
DR   Pfam; PF00045; hemopexin; 4.
DR   Pfam; PF00413; Peptidase_M10; 1.
DR   Pfam; PF03933; Peptidase_M10_N; 1.
DR   PRINTS; PR00138; MATRIXIN.
DR   SMART; SM00120; HX; 4.
DR   SMART; SM00235; ZnMc; 1.
DR   PROSITE; PS00024; HEMOPEXIN; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
DR   PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW   Hydrolase; Metalloprotease; Glycoprotein; Calcium-binding;
KW   Metal-binding; Zinc; Zymogen; Collagen degradation;
KW   Extracellular matrix; Signal.
FT   SIGNAL        1     18       BY SIMILARITY.
FT   PROPEP       19     99       ACTIVATION PEPTIDE.
FT   CHAIN       100    469       INTERSTITIAL COLLAGENASE.
FT   DOMAIN      275    469       HEMOPEXIN-LIKE.
FT   SITE         92     92       CYSTEINE SWITCH (POTENTIAL).
FT   METAL       124    124       CALCIUM 1 (BY SIMILARITY).
FT   METAL       158    158       CALCIUM 2 (BY SIMILARITY).
FT   METAL       168    168       ZINC 1 (BY SIMILARITY).
FT   METAL       170    170       ZINC 1 (BY SIMILARITY).
FT   METAL       175    175       CALCIUM 3 (BY SIMILARITY).
FT   METAL       176    176       CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT                                 SIMILARITY).
FT   METAL       178    178       CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT                                 SIMILARITY).
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FT   METAL       180    180       CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT                                 SIMILARITY).
FT   METAL       183    183       ZINC 1 (BY SIMILARITY).
FT   METAL       190    190       CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
FT                                 SIMILARITY).
FT   METAL       192    192       CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
FT                                 SIMILARITY).
FT   METAL       194    194       CALCIUM 2 (BY SIMILARITY).
FT   METAL       196    196       ZINC 1 (BY SIMILARITY).
FT   METAL       198    198       CALCIUM 3 (BY SIMILARITY).
FT   METAL       199    199       CALCIUM 1 (BY SIMILARITY).
FT   METAL       201    201       CALCIUM 3 (BY SIMILARITY).
FT   METAL       218    218       ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    219    219       BY SIMILARITY.
FT   METAL       222    222       ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT   METAL       228    228       ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT   METAL       285    285       CALCIUM 4 (VIA CARBONYL OXYGEN) (BY
FT                                 SIMILARITY).
FT   METAL       329    329       CALCIUM 4 (VIA CARBONYL OXYGEN) (BY
FT                                 SIMILARITY).
FT   METAL       378    378       CALCIUM 4 (VIA CARBONYL OXYGEN) (BY
FT                                 SIMILARITY).
FT   METAL       427    427       CALCIUM 4 (VIA CARBONYL OXYGEN) (BY
FT                                 SIMILARITY).
FT   DISULFID    278    466       BY SIMILARITY.
SQ   SEQUENCE   469 AA;  54001 MW;  AEE6760AB2C529CA CRC64;

  Query Match              2.6%;  Score 8;  DB 1;  Length 469;
  Best Local Similarity   100.0%;  Pred. No. 9.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 SLPLLLLL 21
              ||||||||
Db          3 SLPLLLLL 10


RESULT 5
BMP1_MOUSE
ID   BMP1_MOUSE     STANDARD;      PRT;   991 AA.
AC   P98063;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
DE   (Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mTld).
GN   BMP1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Embryo;
RX   MEDLINE=94229342; PubMed=8174772;
RA   Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.;
RT   "Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
RT   which is related to the Drosophila dorsoventral gene tolloid and
RT   encodes a putative astacin metalloendopeptidase.";
RL   Dev. Biol. 163:175-183(1994).
CC   -!- FUNCTION: Cleaves the C-terminal propeptides of procollagen I, II
CC       and III. Induces cartilage and bone formation.
CC   -!- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
CC       Ala-|-Asp in type I and II procollagens and at Arg-|-Asp in type
CC       III.
CC   -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC   -!- ENZYME REGULATION: Activity is increased by the procollagen C-
CC       endopeptidase enhancer protein.
CC   -!- TISSUE SPECIFICITY: At high levels in embryonic maternal deciduum
CC       and floor plate region of the neural tube. Less in developing
CC       membranous and endochondral bone, submucosa of intestine, dermis
CC       of skin and the mesenchyme of spleen and lung.
CC   -!- SIMILARITY: Belongs to peptidase family M12A.
CC   -!- SIMILARITY: Contains 2 EGF-like domains
CC   -!- SIMILARITY: Contains 5 CUB domains.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L24755; AAA37306.1; -.
DR   PIR; I49540; I49540.
DR   HSSP; P00736; 1APQ.
DR   MEROPS; M12.005; -.
DR   MGD; MGI:88176; Bmp1.
DR   InterPro; IPR000152; Asx_hydroxyl_S.
DR   InterPro; IPR000859; CUB.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR006026; Peptidase_M.
DR   InterPro; IPR001506; Peptidase_M12A.
DR   Pfam; PF01400; Astacin; 1.
DR   Pfam; PF00431; CUB; 5.
DR   Pfam; PF00008; EGF; 2.
DR   PRINTS; PR00480; ASTACIN.
DR   SMART; SM00042; CUB; 5.
DR   SMART; SM00179; EGF_CA; 2.
DR   SMART; SM00235; ZnMc; 1.
DR   PROSITE; PS00010; ASX_HYDROXYL; 2.
DR   PROSITE; PS01180; CUB; 5.
DR   PROSITE; PS00022; EGF_1; FALSE_NEG.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS50026; EGF_3; 2.
DR   PROSITE; PS01187; EGF_CA; 2.
DR   PROSITE; PS00142; ZINC_PROTEASE; 1.
KW   Growth factor; Cytokine; Repeat; Osteogenesis; Chondrogenesis;
KW   Hydrolase; Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
KW   Glycoprotein; Zymogen.
FT   SIGNAL        1     25       POTENTIAL.
FT   PROPEP       26    125       POTENTIAL.
FT   CHAIN       126    991       BONE MORPHOGENETIC PROTEIN 1.
FT   DOMAIN      126    326       METALLOPROTEASE.
FT   DOMAIN      327    439       CUB 1.
FT   DOMAIN      440    551       CUB 2.
FT   DOMAIN      552    593       EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN      596    707       CUB 3.
FT   DOMAIN      708    748       EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN      752    864       CUB 4.
FT   DOMAIN      865    981       CUB 5.
FT   METAL       218    218       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE    219    219       BY SIMILARITY.
FT   METAL       222    222       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL       228    228       ZINC (CATALYTIC) (BY SIMILARITY).
FT   DISULFID    188    191       BY SIMILARITY.
FT   DISULFID    327    353       BY SIMILARITY.
FT   DISULFID    380    402       BY SIMILARITY.
FT   DISULFID    440    466       BY SIMILARITY.
FT   DISULFID    493    515       BY SIMILARITY.
FT   DISULFID    556    568       BY SIMILARITY.
FT   DISULFID    564    577       BY SIMILARITY.
FT   DISULFID    579    592       BY SIMILARITY.
FT   DISULFID    596    622       BY SIMILARITY.
FT   DISULFID    649    671       BY SIMILARITY.
FT   DISULFID    712    723       BY SIMILARITY.
FT   DISULFID    719    732       BY SIMILARITY.
FT   DISULFID    734    747       BY SIMILARITY.
FT   CARBOHYD     96     96       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    147    147       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    337    337       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    368    368       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    604    604       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   991 AA;  111607 MW;  68A1847783A0BB9E CRC64;
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  Query Match             2.6%;  Score 8;  DB 1;  Length 991;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 SLPLLLLL 21
              ||||||||
Db         13 SLPLLLLL 20


RESULT 6
CYGD_HUMAN
ID   CYGD_HUMAN      STANDARD;      PRT;  1103 AA.
AC   Q02846;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Retinal guanylyl cyclase 1 precursor (EC 4.6.1.2) (Guanylate cyclase
DE   2D, retinal) (RETGC-1) (Rod outer segment membrane guanylate cyclase)
DE   (ROS-GC).
GN   GUCY2D OR GUC2D OR RETGC1 OR RETGC OR GUC1A4 OR CORD6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RX   MEDLINE=93001163; PubMed=1356371;
RA   Shyjan A.W., de Sauvage F.J., Gillett N.A., Goeddel D.V., Lowe D.G.;
RT   "Molecular cloning of a retina-specific membrane guanylyl cyclase.";
RL   Neuron 9:727-737(1992).
RN   [2]
RP   REVISIONS.
RC   TISSUE=Retina;
RA   Lowe D.G.;
RL   Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Perrault I.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   3D-STRUCTURE MODELING OF 871-1028.
RX   MEDLINE=98054247; PubMed=9391039;
RA   Liu Y., Ruoho A.E., Rao V.D., Hurley J.H.;
RT   "Catalytic mechanism of the adenylyl and guanylyl cyclases: modeling
RT   and mutational analysis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:13414-13419(1997).
RN   [5]
RP   VARIANT LCA1 SER-52.
RX   MEDLINE=97099458; PubMed=8944027;
RA   Perrault I., Rozet J.M., Calvas P., Gerber S., Camuzat A.,
RA   Dollfus H., Chatelin S., Souied E., Ghazi I., Leowski C.,
RA   Bonnemaison M., le Paslier D., Frezal J., Dufier J.-L., Pittler S.,
RA   Munnich A., Kaplan J.;
RT   "Retinal-specific guanylate cyclase gene mutations in Leber's
RT   congenital amaurosis.";
RL   Nat. Genet. 14:461-464(1996).
RN   [6]
RP   VARIANT CORD6 837-ASP--MET-839.
RX   MEDLINE=98349989; PubMed=9683616;
RA   Perrault I., Rozet J.-M., Gerber S., Kelsell R.E., Souied E.,
RA   Cabot A., Hunt D.M., Munnich A., Kaplan J.;
RT   "A retGC-1 mutation in autosomal dominant cone-rod dystrophy.";
RL   Am. J. Hum. Genet. 63:651-654(1998).
RN   [7]
RP   VARIANTS CORD6 ASP-837 AND CYS-838.
RX   MEDLINE=98282246; PubMed=9618177;
RA   Kelsell R.E., Gregory-Evans K., Payne A.M., Perrault I., Kaplan J.,
RA   Yang R.-B., Garbers D.L., Bird A.C., Moore A.T., Hunt D.M.;
RT   "Mutations in the retinal guanylate cyclase (RETGC-1) gene in dominant
RT   cone-rod dystrophy.";
RL   Hum. Mol. Genet. 7:1179-1184(1998).
RN   [8]
RP   CHARACTERIZATION OF VARIANT SER-565.
RX   MEDLINE=99105799; PubMed=9888789;
RA   Duda T., Venkataraman V., Goraczniak R., Lange C., Koch K.-W.,
RA   Sharma R.K.;
RT   "Functional consequences of a rod outer segment membrane guanylate
RT   cyclase (ROS-GC1) gene mutation linked with Leber's congenital
RT   amaurosis.";
RL   Biochemistry 38:509-515(1999).
RN   [9]
RP   VARIANTS CORD5 CYS-838 AND HIS-838.
RX   MEDLINE=22439680; PubMed=12552567;
RA   Udar N., Yelchits S., Chalukya M., Yellore V., Nusinowitz S.,
RA   Silva-Garcia R., Vrabec T., Hussles Maumenee I., Donoso L.,
RA   Small K.W.;
RT   "Identification of GUCY2D gene mutations in CORD5 families and
RT   evidence of incomplete penetrance.";
RL   Hum. Mutat. 21:170-171(2003).
CC   -!- FUNCTION: PROBABLY PLAYS A SPECIFIC FUNCTIONAL ROLE IN THE RODS
CC       AND/OR CONES OF PHOTORECEPTORS. IT MAY BE THE ENZYME INVOLVED IN
CC       THE RESYNTHESIS OF CGMP REQUIRED FOR RECOVERY OF THE DARK STATE
CC       AFTER PHOTOTRANSDUCTION.
CC   -!- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.
CC   -!- ENZYME REGULATION: Activated by GCAP-1; inhibited by calcium.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Retina. Localized exclusively in the nuclei
CC       and inner segments of the rod and cone photoreceptor cells.
CC   -!- DISEASE: Defects in GUCY2D are a cause of Leber congenital
CC       amaurosis type 1 (LCA1) [MIM:204000]. It is characterized by total
CC       blindness or greatly impaired vision with loss of central vision.
CC   -!- DISEASE: Defects in GUCY2D are a cause of dominant cone-rod
CC       dystrophy type 6 (CORD6) [MIM:601777]. It is characterized by the
CC       initial degeneration of cone photoreceptor cells, causing early
CC       loss of visual acuity and color vision, followed by the
CC       degeneration of rod photoreceptor cells leading to progressive
CC       night blindness and peripheral visual field loss. The disease
CC       displays phenotypic heterogeneity and different gene locis are
CC       involved.
CC   -!- DISEASE: Defects in GUCY2D are a cause of dominant cone-rod
CC       dystrophy type 5 (CORD5) [MIM:600977]. It seems to be a variant of
CC       CORD6.
CC   -!- SIMILARITY: Belongs to the adenylyl cyclase class-4/guanylyl
CC       cyclase family.
CC   -!- SIMILARITY: Contains 1 protein kinase-like domain.
CC   -!- DATABASE: NAME=Mutations of the GUCY2D gene;
CC       NOTE=Retina International's Scientific Newsletter;
CC       WWW="http://www.retina-international.com/sci-news/gcmut.htm".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M92432; AAA60547.1; -.
DR   EMBL; AJ222657; CAA10914.1; -.
DR   PIR; JH0717; JH0717.
DR   PDB; 1AWL; 28-JAN-98.
DR   Genew; HGNC:4689; GUCY2D.
DR   MIM; 600179; -.
DR   MIM; 204000; -.
DR   MIM; 601777; -.
DR   MIM; 600977; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005640; C:nuclear outer membrane; TAS.
DR   GO; GO:0004383; F:guanylate cyclase activity; TAS.
DR   GO; GO:0008075; F:receptor guanylate cyclase activity; TAS.
DR   GO; GO:0007168; P:receptor guanylyl cyclase signaling pathway; TAS.
DR   GO; GO:0007601; P:vision; TAS.
DR   InterPro; IPR001828; ANF_receptor.
DR   InterPro; IPR001054; G_cyclase.
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DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF01094; ANF_receptor; 1.
DR   Pfam; PF00211; guanylate_cyc; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00044; CYCc; 1.
DR   PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
DR   PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Lyase; cGMP biosynthesis; Signal; Transmembrane; Vision; Glycoprotein;
KW   Multigene family; Disease mutation; Cone-rod dystrophy; Polymorphism;
KW   3D-structure.
FT   SIGNAL        1     51       POTENTIAL.
FT   CHAIN        52   1103       RETINAL GUANYLYL CYCLASE 1.
FT   DOMAIN       52    462       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    463    487       POTENTIAL.
FT   DOMAIN      488   1103       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      525    808       PROTEIN KINASE-LIKE.
FT   DOMAIN      880   1010       GUANYLATE CYCLASE.
FT   DISULFID    449    449       INTERCHAIN (PROBABLE).
FT   DISULFID    457    457       INTERCHAIN (PROBABLE).
FT   CARBOHYD    297    297       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      52     52       A -> S (in LCA1; could be a rare
FT                                polymorphism).
FT                                /FTId=VAR_003435.
FT   VARIANT     274    274       V -> P (in LCA1).
FT                                /FTId=VAR_009128.
FT   VARIANT     362    362       A -> S (in LCA1).
FT                                /FTId=VAR_009129.
FT   VARIANT     565    565       F -> S (in LCA1; loss of activity).
FT                                /FTId=VAR_009131.
FT   VARIANT     573    573       I -> V (in LCA1).
FT                                /FTId=VAR_009130.
FT   VARIANT     701    701       P -> S (in LCA1).
FT                                /FTId=VAR_009132.
FT   VARIANT     782    782       L -> H (rare polymorphism).
FT                                /FTId=VAR_009133.
FT   VARIANT     837    837       E -> D (in CORD6).
FT                                /FTId=VAR_003436.
FT   VARIANT     837    839       ERT -> DCM (in CORD6).
FT                                /FTId=VAR_003438.
FT   VARIANT     838    838       R -> C (in CORD6 and CORD5).
FT                                /FTId=VAR_003437.
FT   VARIANT     838    838       R -> H (in CORD5).
FT                                /FTId=VAR_015373.
FT   VARIANT     858    858       P -> S (in LCA1).
FT                                /FTId=VAR_009134.
FT   VARIANT     954    954       L -> P (in LCA1).
FT                                /FTId=VAR_009135.
FT   STRAND      874    874
FT   STRAND      879    879
FT   STRAND      882    885
FT   TURN        887    887
FT   HELIX       888    892
FT   HELIX       899    902
FT   TURN        903    903
FT   HELIX       904    913
FT   TURN        914    917
FT   STRAND      921    922
FT   STRAND      927    927
FT   TURN        928    929
FT   STRAND      930    931
FT   STRAND      934    935
FT   TURN        937    938

  Query Match             2.6%;  Score 8;  DB 1;  Length 1103;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 LLLLQPPA 95
              ||||||||
Db         42 LLLLQPPA 49


RESULT 7
PTPF_HUMAN
ID   PTPF_HUMAN     STANDARD;      PRT;  1897 AA.
AC   P10586;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   LAR protein precursor (Leukocyte antigen related) (EC 3.1.3.48).
GN   PTPRF OR LAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tonsil;
RX   MEDLINE=89035978; PubMed=2972792;
RA   Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.;
RT   "A new member of the immunoglobulin superfamily that has a
RT   cytoplasmic region homologous to the leukocyte common antigen.";
RL   J. Exp. Med. 168:1523-1530(1988).
RN   [2]
RP   MUTAGENESIS.
RX   MEDLINE=90046860; PubMed=2554325;
RA   Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
RT   "A family of receptor-linked protein tyrosine phosphatases in humans
RT   and Drosophila.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
RN   [3]
RP   MUTAGENESIS.
RX   MEDLINE=90316093; PubMed=1695146;
RA   Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;
RT   "Distinct functional roles of the two intracellular phosphatase like
RT   domains of the receptor-linked protein tyrosine phosphatases LCA and
RT   LAR.";
RL   EMBO J. 9:2399-2407(1990).
CC   -!- FUNCTION: It is possible that DLAR is a cell adhesion receptor.
CC       It possesses an intrinsic protein tyrosine phosphatase activity
CC       (PTPase).
CC   -!- FUNCTION: The first PTPase domain has enzymatic activity, while
CC       the second one seems to affect the substrate specificity of the
CC       first one.
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 8 fibronectin type III domains.
CC   -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y00815; CAA68754.1; -.
DR   PIR; S03841; TDHULK.
DR   PDB; 1LAR; 25-APR-00.
DR   Genew; HGNC:9670; PTPRF.
DR   MIM; 179590; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
DR   GO; GO:0007155; P:cell adhesion; TAS.
DR   GO; GO:0007185; P:transmembrane receptor protein tyrosine pho. . .; TAS.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003962; FnIII_subd.
DR   InterPro; IPR007110; Ig-like.
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DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00041; fn3; 7.
DR   Pfam; PF00047; ig; 3.
DR   Pfam; PF00102; Y_phosphatase; 2.
DR   PRINTS; PR00014; FNTYPEIII.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00060; FN3; 4.
DR   SMART; SM00408; IGc2; 3.
DR   SMART; SM00194; PTPc; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW   Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
KW   Cell adhesion; Immunoglobulin domain; Repeat; 3D-structure.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17   1897       LAR PROTEIN.
FT   DOMAIN       17   1250       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1251   1274       POTENTIAL.
FT   DOMAIN     1275   1897       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       23    113       IG-LIKE C2-TYPE 1.
FT   DOMAIN      125    214       IG-LIKE C2-TYPE 2.
FT   DOMAIN      222    304       IG-LIKE C2-TYPE 3.
FT   DOMAIN     1360   1606       PROTEIN-TYROSINE PHOSPHATASE 1.
FT   DOMAIN     1649   1897       PROTEIN-TYROSINE PHOSPHATASE 2.
FT   ACT_SITE   1538   1538       PHOSPHOCYSTEINE INTERMEDIATE (BY
FT                                SIMILARITY).
FT   ACT_SITE   1829   1829       PHOSPHOCYSTEINE INTERMEDIATE (BY
FT                                SIMILARITY).
FT   CARBOHYD    107    107       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    240    240       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    285    285       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    711    711       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    956    956       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MUTAGEN    1538   1538       C->S: LOSS OF ACTIVITY.
SQ   SEQUENCE   1897 AA;  211844 MW;  439850F1D5C031FF CRC64;

  Query Match             2.6%;  Score 8;  DB 1;  Length 1897;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        207 CVATNSAG 214
              ||||||||
Db        197 CVATNSAG 204


RESULT 8
PTPD_HUMAN
ID   PTPD_HUMAN     STANDARD;      PRT;  1912 AA.
AC   P23468;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-
DE   delta).
GN   PTPRD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.
RX   MEDLINE=95204468; PubMed=7896816;
RA   Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;
RT   "Molecular characterization of the human transmembrane protein-
RT   tyrosine phosphatase delta. Evidence for tissue-specific expression of
RT   alternative human transmembrane protein-tyrosine phosphatase delta
RT   isoforms.";
RL   J. Biol. Chem. 270:6722-6728(1995).
RN   [2]
RP   SEQUENCE OF 390-1912 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=91006018; PubMed=2170109;
RA   Krueger N.X., Streuli M., Saito H.;
RT   "Structural diversity and evolution of human receptor-like protein
RT   tyrosine phosphatases.";
RL   EMBO J. 9:3241-3252(1990).
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1;
CC         IsoId=P23468-1; Sequence=Displayed;
CC       Name=2; Synonyms=Kidney;
CC         IsoId=P23468-2; Sequence=VSP_005147, VSP_005148, VSP_005149;
CC       Name=3; Synonyms=Fetal brain;
CC         IsoId=P23468-3; Sequence=VSP_005150;
CC   -!- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
CC       FROM THE TRANSMEMBRANE SEGMENT.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 8 fibronectin type III domains.
CC   -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L38929; AAC41749.1; -.
DR   EMBL; X54133; CAA38068.1; -.
DR   PIR; A56178; A56178.
DR   HSSP; P18052; 1YFO.
DR   Genew; HGNC:9668; PTPRD.
DR   MIM; 601598; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
DR   GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR   GO; GO:0007185; P:transmembrane receptor protein tyrosine pho. . .; TAS.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003962; FnIII_subd.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00041; fn3; 8.
DR   Pfam; PF00047; ig; 3.
DR   Pfam; PF00102; Y_phosphatase; 2.
DR   PRINTS; PR00014; FNTYPEIII.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00060; FN3; 8.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00194; PTPc; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW   Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21   1912       PROTEIN-TYROSINE PHOSPHATASE DELTA.
FT   DOMAIN       21   1265       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1266   1290       POTENTIAL.
FT   DOMAIN     1291   1912       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       24    114       IG-LIKE C2-TYPE 1.
FT   DOMAIN      126    224       IG-LIKE C2-TYPE 2.
FT   DOMAIN      236    318       IG-LIKE C2-TYPE 3.
FT   DOMAIN      320    414       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      417    513       FIBRONECTIN TYPE-III 2.
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FT   DOMAIN       516    606       FIBRONECTIN TYPE-III 3.
FT   DOMAIN       609    708       FIBRONECTIN TYPE-III 4.
FT   DOMAIN       711    822       FIBRONECTIN TYPE-III 5.
FT   DOMAIN       825    916       FIBRONECTIN TYPE-III 6.
FT   DOMAIN       918   1017       FIBRONECTIN TYPE-III 7.
FT   DOMAIN      1020   1137       FIBRONECTIN TYPE-III 8.
FT   DOMAIN      1375   1618       PROTEIN-TYROSINE PHOSPHATASE 1.
FT   DOMAIN      1619   1912       PROTEIN-TYROSINE PHOSPHATASE 2.
FT   ACT_SITE    1553   1553       PHOSPHOCYSTEINE INTERMEDIATE (BY
FT                                 SIMILARITY).
FT   ACT_SITE    1844   1844       PHOSPHOCYSTEINE INTERMEDIATE (BY
FT                                 SIMILARITY).
FT   SITE        1175   1178       CLEAVAGE (POTENTIAL).
FT   CARBOHYD     254    254       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     299    299       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     724    724       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     832    832       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     181    189       Missing (in isoform 2).
FT                                 /FTId=VSP_005147.
FT   VARSPLIC     226    229       Missing (in isoform 2).
FT                                 /FTId=VSP_005148.
FT   VARSPLIC     775    783       Missing (in isoform 2).
FT                                 /FTId=VSP_005149.
FT   VARSPLIC     609   1137       Missing (in isoform 3).
FT                                 /FTId=VSP_005150.
FT   MUTAGEN     1178   1178       R->A: 2.5-FOLD REDUCTION IN CLEAVAGE.
SQ   SEQUENCE   1912 AA;  214759 MW;  3AE8CBCD32182E26 CRC64;

  Query Match              2.6%;  Score 8;  DB 1;  Length 1912;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        207 CVATNSAG 214
              ||||||||
Db        207 CVATNSAG 214


RESULT 9
PTNS_HUMAN
ID   PTNS_HUMAN     STANDARD;      PRT;  1948 AA.
AC   Q13332; Q15718; Q16341;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Receptor-type protein-tyrosine phosphatase S precursor (EC 3.1.3.48)
DE   (R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).
GN   PTPRS.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal brain;
RX   MEDLINE=96102179; PubMed=8524829;
RA   Pulido R., Serra-Pages C., Tang M., Streuli M.;
RT   "The LAR/PTP delta/PTP sigma subfamily of transmembrane protein-
RT   tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sigma
RT   isoforms are expressed in a tissue-specific manner and associate with
RT   the LAR-interacting protein LIP.1.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96255038; PubMed=8992885;
RA   Endo N., Rutledge S.J., Opas E.E., Vogel R., Rodan G.A., Schmidt A.;
RT   "Human protein tyrosine phosphatase-sigma: alternative splicing and
RT   inhibition by bisphosphonates.";
RL   J. Bone Miner. Res. 11:535-543(1996).
RN   [3]
RP   SEQUENCE OF 1-126 FROM N.A.
RA   Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA   Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA   Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA   Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA   Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
RA   Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA   Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA   Olsen A.S., Carrano A.V.;
RT   "Sequence analysis of a 2.5 Mb region in 19p13.3.";
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1503-1589 FROM N.A.
RX   MEDLINE=92119637; PubMed=1370651;
RA   Adachi M., Sekiya M., Arimura Y., Takekawa M., Itoh F., Hinoda Y.,
RA   Imai K., Yachi A.;
RT   "Protein-tyrosine phosphatase expression in pre-B cell NALM-6.";
RL   Cancer Res. 52:737-740(1992).
CC   -!- FUNCTION: Interacts with LAR-interacting protein LIP.1.
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=5;
CC         Comment=Additional isoforms seem to exist;
CC       Name=PTPS;
CC         IsoId=Q13332-1; Sequence=Displayed;
CC       Name=PTPS-MEA;
CC         IsoId=Q13332-2; Sequence=VSP_050021;
CC       Name=PTPS-MEB;
CC         IsoId=Q13332-3; Sequence=VSP_050022, VSP_050026, VSP_050027;
CC       Name=PTPS-MEC;
CC         IsoId=Q13332-4; Sequence=VSP_050024;
CC       Name=PTPS-F4-7;
CC         IsoId=Q13332-5; Sequence=VSP_050023, VSP_050025;
CC   -!- TISSUE SPECIFICITY: DEtected in all tissues tested except for
CC       placenta and liver.
CC   -!- SIMILARITY: BELONGS TO THE RECEPTOR CLASS OF THE PROTEIN-TYROSINE
CC       PHOSPHATASE FAMILY.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.
CC   -!- SIMILARITY: Contains 8 fibronectin type III domains.
CC   -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   EMBL; U35234; AAC50299.1; -.
DR   EMBL; U40317; AAC50567.1; -.
DR   EMBL; AC005790; AAC62832.1; -.
DR   EMBL; S78080; AAB21146.2; -.
DR   HSSP; P18052; 1YFO.
DR   Genew; HGNC:9681; PTPRS.
DR   MIM; 601576; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003962; FnIII_subd.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00041; fn3; 8.
DR   Pfam; PF00047; ig; 3.
DR   Pfam; PF00102; Y_phosphatase; 2.
DR   PRINTS; PR00014; FNTYPEIII.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00060; FN3; 7.
DR   SMART; SM00408; IGc2; 3.
DR   SMART; SM00194; PTPc; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
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DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW   Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
KW   Cell adhesion; Immunoglobulin domain; Alternative splicing; Repeat.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30   1948       RECEPTOR-TYPE PROTEIN-TYROSINE
FT                                PHOSPHATASE S.
FT   DOMAIN       30   1282       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1283   1303       POTENTIAL.
FT   DOMAIN     1304   1948       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       33    123       IG-LIKE C2-TYPE 1.
FT   DOMAIN      135    233       IG-LIKE C2-TYPE 2.
FT   DOMAIN      245    327       IG-LIKE C2-TYPE 3.
FT   DOMAIN      329    423       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      426    522       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      525    615       FIBRONECTIN TYPE-III 3.
FT   DOMAIN      618    717       FIBRONECTIN TYPE-III 4.
FT   DOMAIN      720    831       FIBRONECTIN TYPE-III 5.
FT   DOMAIN      834    926       FIBRONECTIN TYPE-III 6.
FT   DOMAIN      928   1033       FIBRONECTIN TYPE-III 7.
FT   DOMAIN     1036   1151       FIBRONECTIN TYPE-III 8.
FT   DOMAIN     1393   1648       PROTEIN-TYROSINE PHOSPHATASE 1.
FT   DOMAIN     1680   1930       PROTEIN-TYROSINE PHOSPHATASE 2.
FT   DOMAIN      641    644       POLY-PRO.
FT   DISULFID     54    107       POTENTIAL.
FT   DISULFID    156    216       POTENTIAL.
FT   DISULFID    266    311       POTENTIAL.
FT   ACT_SITE   1589   1589       PHOSPHOCYSTEINE INTERMEDIATE (BY
FT                                SIMILARITY).
FT   ACT_SITE   1880   1880       PHOSPHOCYSTEINE INTERMEDIATE (BY
FT                                SIMILARITY).
FT   CARBOHYD    263    263       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    308    308       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    733    733       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    940    940       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    190    198       Missing (in isoform PTPS-MEA).
FT                                /FTId=VSP_050021.
FT   VARSPLIC    236    239       Missing (in isoform PTPS-MEB).
FT                                /FTId=VSP_050022.
FT   VARSPLIC    617   1034       Missing (in isoform PTPS-F4-7).
FT                                /FTId=VSP_050023.
FT   VARSPLIC    784    792       Missing (in isoform PTPS-MEC).
FT                                /FTId=VSP_050024.
FT   VARSPLIC   1035   1035       V -> I (in isoform PTPS-F4-7).
FT                                /FTId=VSP_050025.
FT   VARSPLIC   1350   1365       Missing (in isoform PTPS-MEB).
FT                                /FTId=VSP_050026.
FT   VARSPLIC   1366   1366       S -> G (in isoform PTPS-MEB).
FT                                /FTId=VSP_050027.
FT   CONFLICT    310    310       T -> HP (IN REF. 2).
FT   CONFLICT    428    429       SA -> RP (IN REF. 2).
FT   CONFLICT    742    745       LGPV -> RSPA (IN REF. 2).
FT   CONFLICT    765    773       GAEGRGPPR -> RREARGRRS (IN REF. 2).
FT   CONFLICT    910    910       R -> P (IN REF. 2).
FT   CONFLICT    986    995       AAEPGAENAV -> GRLSRARRTL (IN REF. 2).
FT   CONFLICT   1195   1196       TV -> SL (IN REF. 2).
FT   CONFLICT   1431   1431       F -> S (IN REF. 2).
FT   CONFLICT   1546   1546       E -> D (IN REF. 4).
FT   CONFLICT   1587   1587       V -> A (IN REF. 4).
FT   CONFLICT   1705   1705       N -> K (IN REF. 2).
SQ   SEQUENCE   1948 AA;  217080 MW;  7DC049EC03171136 CRC64;

  Query Match             2.6%;  Score 8;  DB 1;  Length 1948;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        207 CVATNSAG 214
              ||||||||
Db        216 CVATNSAG 223


RESULT 10
UN89_CAEEL
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ID   UN89_CAEEL     STANDARD;      PRT;  6632 AA.
AC   O01761; Q17362;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Muscle M-line assembly protein unc-89 (Uncoordinated protein 89).
GN   UNC-89 OR C09D1.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC   STRAIN=Bristol N2;
RX   MEDLINE=96180278; PubMed=8603916;
RA   Benian G.M., Tinley T.L., Tang X., Borodovsky M.;
RT   "The Caenorhabditis elegans gene unc-89, required for muscle M-line
RT   assembly, encodes a giant modular protein composed of Ig and signal
RT   transduction domains.";
RL   J. Cell Biol. 132:835-848(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Du Z., Le T.T., Wilson R.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   REVISIONS.
RA   Waterston R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Structural component of the muscle M-line. Myofilament
CC       lattice assembly begins with positional cues laid down in the
CC       basement membrane and muscle cell membrane. UNC-89 responds to
CC       these signals, localizes, and then participates in assembling an
CC       M-line.
CC   -!- TISSUE SPECIFICITY: Localizes to the middle of A-bands.
CC   -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
CC   -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC   -!- SIMILARITY: Contains 49 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 1 PH domain.
CC   -!- SIMILARITY: Contains 5 RCSD domains.
CC   -!- SIMILARITY: Contains 1 SH3 domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U33058; AAB00542.1; -.
DR   EMBL; AF003131; AAB54132.2; -.
DR   PDB; 1FHO; 20-DEC-00.
DR   WormPep; C09D1.1; CE30426.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR007850; RCSD.
DR   InterPro; IPR000219; RhoGEF.
DR   InterPro; IPR001452; SH3.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 47.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF05177; RCSD; 5.
DR   Pfam; PF00621; RhoGEF; 1.
DR   Pfam; PF00018; SH3; 1.
DR   SMART; SM00408; IGc2; 23.
DR   SMART; SM00325; RhoGEF; 1.
DR   SMART; SM00326; SH3; 1.
DR   PROSITE; PS50010; DH_2; 1.
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DR   PROSITE; PS50835; IG_LIKE; 49.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
DR   PROSITE; PS50002; SH3; 1.
KW   Muscle protein; Immunoglobulin domain; Repeat; SH3 domain;
KW   3D-structure.
FT   DOMAIN       63     127       SH3.
FT   DOMAIN      152     330       DH.
FT   DOMAIN      342     498       PH.
FT   DOMAIN      547     633       IG-LIKE C2-TYPE 1.
FT   DOMAIN      648     736       IG-LIKE C2-TYPE 2.
FT   DOMAIN      748     838       IG-LIKE C2-TYPE 3.
FT   DOMAIN      946    1033       IG-LIKE C2-TYPE 4.
FT   DOMAIN     1044    1132       IG-LIKE C2-TYPE 5.
FT   DOMAIN     1140    1227       IG-LIKE C2-TYPE 6.
FT   DOMAIN     1272    1315       THR-RICH.
FT   DOMAIN     1375    1475       RCSD 1.
FT   DOMAIN     1479    1585       RCSD 2.
FT   DOMAIN     1597    1695       RCSD 3.
FT   DOMAIN     1700    1799       RCSD 4.
FT   DOMAIN     1800    1860       RCSD 5.
FT   DOMAIN     1982    2067       IG-LIKE C2-TYPE 7.
FT   DOMAIN     2071    2163       IG-LIKE C2-TYPE 8.
FT   DOMAIN     2171    2261       IG-LIKE C2-TYPE 9.
FT   DOMAIN     2269    2359       IG-LIKE C2-TYPE 10.
FT   DOMAIN     2367    2455       IG-LIKE C2-TYPE 11.
FT   DOMAIN     2463    2564       IG-LIKE C2-TYPE 12.
FT   DOMAIN     2563    2651       IG-LIKE C2-TYPE 13.
FT   DOMAIN     2657    2746       IG-LIKE C2-TYPE 14.
FT   DOMAIN     2754    2858       IG-LIKE C2-TYPE 15.
FT   DOMAIN     2887    2980       IG-LIKE C2-TYPE 16.
FT   DOMAIN     2994    3081       IG-LIKE C2-TYPE 17.
FT   DOMAIN     3087    3183       IG-LIKE C2-TYPE 18.
FT   DOMAIN     3189    3280       IG-LIKE C2-TYPE 19.
FT   DOMAIN     3286    3376       IG-LIKE C2-TYPE 20.
FT   DOMAIN     3384    3469       IG-LIKE C2-TYPE 21.
FT   DOMAIN     3482    3572       IG-LIKE C2-TYPE 22.
FT   DOMAIN     3580    3667       IG-LIKE C2-TYPE 23.
FT   DOMAIN     3686    3777       IG-LIKE C2-TYPE 24.
FT   DOMAIN     3817    3908       IG-LIKE C2-TYPE 25.
FT   DOMAIN     3920    4009       IG-LIKE C2-TYPE 26.
FT   DOMAIN     4018    4106       IG-LIKE C2-TYPE 27.
FT   DOMAIN     4109    4201       IG-LIKE C2-TYPE 28.
FT   DOMAIN     4212    4297       IG-LIKE C2-TYPE 29.
FT   DOMAIN     4302    4387       IG-LIKE C2-TYPE 30.
FT   DOMAIN     4400    4485       IG-LIKE C2-TYPE 31.
FT   DOMAIN     4489    4580       IG-LIKE C2-TYPE 32.
FT   DOMAIN     4588    4678       IG-LIKE C2-TYPE 33.
FT   DOMAIN     4681    4771       IG-LIKE C2-TYPE 34.
FT   DOMAIN     4873    4961       IG-LIKE C2-TYPE 35.
FT   DOMAIN     4965    5057       IG-LIKE C2-TYPE 36.
FT   DOMAIN     5067    5160       IG-LIKE C2-TYPE 37.
FT   DOMAIN     5171    5260       IG-LIKE C2-TYPE 38.
FT   DOMAIN     5277    5366       IG-LIKE C2-TYPE 39.
FT   DOMAIN     5383    5472       IG-LIKE C2-TYPE 40.
FT   DOMAIN     5487    5578       IG-LIKE C2-TYPE 41.
FT   DOMAIN     5595    5685       IG-LIKE C2-TYPE 42.
FT   DOMAIN     5701    5790       IG-LIKE C2-TYPE 43.
FT   DOMAIN     5815    5904       IG-LIKE C2-TYPE 44.
FT   DOMAIN     5925    6014       IG-LIKE C2-TYPE 45.
FT   DOMAIN     6038    6130       IG-LIKE C2-TYPE 46.
FT   DOMAIN     6150    6239       IG-LIKE C2-TYPE 47.
FT   DOMAIN     6275    6368       FIBRONECTIN TYPE-III.
FT   DOMAIN     6413    6502       IG-LIKE C2-TYPE 48.
FT   DOMAIN     6507    6596       IG-LIKE C2-TYPE 49.
FT   DISULFID    568     621       POTENTIAL.
FT   DISULFID   2908    2975       POTENTIAL.
FT   DISULFID   3015    3065       POTENTIAL.
FT   DISULFID   3707    3759       POTENTIAL.
FT   DISULFID   3826    3890       POTENTIAL.
FT   DISULFID   5092    5157       POTENTIAL.
FT   DISULFID   5298    5350       POTENTIAL.
FT   DISULFID   5508    5560       POTENTIAL.
FT   DISULFID   5616    5669       POTENTIAL.
FT   DISULFID   5722    5764       POTENTIAL.
FT   DISULFID   5836    5901       POTENTIAL.
FT   DISULFID   5946    5998       POTENTIAL.
FT   DISULFID   6036    6171       POTENTIAL.
FT   DISULFID   6421    6486       POTENTIAL.
FT   CONFLICT   2137    2137       A -> P (IN REF. 1).
FT   CONFLICT   2245    2247       AKA -> PKP (IN REF. 1).
FT   CONFLICT   2258    2258       A -> P (IN REF. 1).
FT   CONFLICT   2284    2284       E -> G (IN REF. 1).
FT   CONFLICT   2297    2297       M -> I (IN REF. 1).
FT   CONFLICT   3531    3531       A -> G (IN REF. 1).
FT   CONFLICT   3884    3888       DAGEY -> RRRRI (IN REF. 1).
FT   CONFLICT   3929    3929       A -> V (IN REF. 1).
FT   CONFLICT   5134    5134       A -> P (IN REF. 1).
FT   CONFLICT   5145    5145       T -> S (IN REF. 1).
FT   CONFLICT   5185    5185       G -> A (IN REF. 1).
FT   CONFLICT   5199    5199       K -> N (IN REF. 1).
FT   CONFLICT   5202    5202       L -> F (IN REF. 1).
FT   CONFLICT   5213    5213       F -> L (IN REF. 1).
FT   CONFLICT   6178    6178       A -> G (IN REF. 1).
FT   CONFLICT   6268    6268       K -> E (IN REF. 1).
SQ   SEQUENCE   6632 AA;  731665 MW;  262D3EDD62960E89 CRC64;

  Query Match             2.6%;  Score 8;  DB 1;  Length 6632;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          65 WLLNGQPL 72
               ||||||||
Db        2205 WLLNGQPL 2212


RESULT 11
NU6M_ALBTU
ID   NU6M_ALBTU     STANDARD;      PRT;    96 AA.
AC   Q08084;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-FEB-1996 (Rel. 33, Last annotation update)
DE   NADH-ubiquinone oxidoreductase chain 6 (EC 1.6.5.3) (Fragment).
GN   ND6.
OS   Albinaria turrita (Door snail).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC   Sigmurethra; Clausilioidea; Clausiliidae; Alopiinae; Albinaria.
OX   NCBI_TaxID=27820;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94275881; PubMed=8007005;
RA   Lecanidou R., Douris V., Rodakis G.C.;
RT   "Novel features of metazoan mtDNA revealed from sequence analysis of
RT   three mitochondrial DNA segments of the land snail Albinaria turrita
RT   (Gastropoda: Clausiliidae).";
RL   J. Mol. Evol. 38:369-382(1994).
CC   -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X71394; CAA50516.1; -.
DR   PIR; S33145; S33145.
KW   Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
FT   NON_TER      96     96
SQ   SEQUENCE   96 AA;  10896 MW;  A1732AACC4FADA4F CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 96;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          17 LLLLLIM 23
               |||||||
Db          27 LLLLLIM 33


RESULT 12
APC2_CAVPO
ID   APC2_CAVPO     STANDARD;      PRT;   100 AA.
AC   P27916;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Apolipoprotein C-II precursor (Apo-CII).
GN   APOC2.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91154195; PubMed=1999402;
RA   Andersson Y., Thelander L., Bengtsson-Olivecrona G.;
RT   "Demonstration of apolipoprotein CII in guinea pigs. Functional
RT   characteristics, cDNA sequence, and tissue expression.";
RL   J. Biol. Chem. 266:4074-4080(1991).
CC   -!- FUNCTION: Component of the very low density lipoprotein (VLDL)
CC       fraction in plasma, and is an activator of several triacylglycerol
CC       lipases. The association of APOC2 with plasma chylomicrons,
CC       VLDL, and HDL is reversible, a function of the secretion and
CC       catabolism of triglyceride-rich lipoproteins, and changes rapidly.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Secreted in plasma.
CC   -!- SIMILARITY: Belongs to the apolipoprotein C2 family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M59913; AAA37031.1; -.
DR   PIR; A38685; A38685.
DR   InterPro; IPR008019; Apo-CII.
DR   Pfam; PF05355; Apo-CII; 1.
KW   Chylomicron; VLDL; Transport; Lipid transport; Lipid degradation;
KW   Signal.
FT   SIGNAL        1     25
FT   CHAIN        26    100       APOLIPOPROTEIN C-II.
SQ   SEQUENCE   100 AA;  10984 MW;  BBCF8DB52FC9E9BD CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          15 LPLLLLL 21
               |||||||
Db          13 LPLLLLL 19


RESULT 13
SZ06_BOVIN
ID   SZ06_BOVIN     STANDARD;      PRT;   112 AA.
AC   P80221; Q9GKP5;
DT   01-FEB-1994 (Rel. 28, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Small inducible cytokine B6 precursor (CXCL6) (Granulocyte chemotactic
DE   protein 2) (GCP-2).
GN   CXCL6 OR SCYB6 OR GCP2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Endometrium;
RA   Austin K.J., Perry D.J., Hansen T.R.;
RT   "The bovine granulocyte chemotactic protein-2 cDNA.";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 37-111.
RC   TISSUE=Kidney;
RX   MEDLINE=94001982; PubMed=8399143;
RA   Proost P., Wuyts A., Conings R., Lenaerts J.-P., Billiau A.,
RA   Opdenakker G., van Damme J.;
RT   "Human and bovine granulocyte chemotactic protein-2: complete amino
RT   acid sequence and functional characterization as chemokines.";
RL   Biochemistry 32:10170-10177(1993).
CC   -!- FUNCTION: Chemotactic for neutrophil granulocytes.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- DEVELOPMENTAL STAGE: Expressed in high amounts from endometria of
CC       day 18-21 pregnant cows.
CC   -!- INDUCTION: By interferon tau and phorbol ester.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF149249; AAG35212.1; -.
DR   HSSP; P02775; 1NAP.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00437; SMALLCYTKCXC.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW   Cytokine; Chemotaxis; Heparin-binding; Signal.
FT   SIGNAL        1     36
FT   CHAIN        37    112       SMALL INDUCIBLE CYTOKINE B6.
FT   DISULFID     48     74       BY SIMILARITY.
FT   DISULFID     50     90       BY SIMILARITY.
FT   VARIANT      37     38       MISSING (N-TERMINAL PROCESSING VARIANT).
FT   VARIANT      37     43       MISSING (N-TERMINAL PROCESSING VARIANT).
FT   VARIANT      37     44       MISSING (N-TERMINAL PROCESSING VARIANT).
FT   VARIANT      37     45       MISSING (N-TERMINAL PROCESSING VARIANT).
SQ   SEQUENCE   112 AA;  11589 MW;  6ED8148B96A7C082 CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 112;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         218 SRAARVS 224
               |||||||
Db           6 SRAARVS 12


RESULT 14
RMP3_MOUSE
ID   RMP3_MOUSE     STANDARD;      PRT;   147 AA.
AC   Q9WUP1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Receptor activity-modifying protein 3 precursor.
GN   RAMP3.
OS   Mus musculus (Mouse).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Derst C., Preisig-Mueller R., Gerhardus J., Daut J.;
RT   "Cloning and sequencing of mouse CGRP/adrenomedullin receptor
RT   subunits.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Husmann K., Sexton P.M., Fischer J.A., Born W.;
RT   "Mouse receptor activity modifying proteins 1, -2 and -3: amino acid
RT   sequence, expression and function.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Lung;
RA   Ono Y., Okano I., Kojima M., Okada K., Kangawa K.;
RT   "cDNA cloning of mouse CRLR and RAMPs.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Required to transport calcitonin-receptor-like receptor
CC       (CRLR) to the plasma membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the RAMP family.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF146524; AAD35020.1; -.
DR   EMBL; AJ250491; CAB59513.1; -.
DR   EMBL; AF209907; AAF21039.1; -.
DR   EMBL; BC024765; AAH24765.1; -.
DR   MGD; MGI:1860292; Ramp3.
DR   GO; GO:0015027; F:coreceptor, soluble ligand activity; IDA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IPI.
DR   InterPro; IPR006985; RAMP.
DR   Pfam; PF04901; RAMP; 1.
KW   Signal; Transmembrane; Transport; Receptor.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    147       RECEPTOR ACTIVITY-MODIFYING PROTEIN 3.
FT   DOMAIN       23    117       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    118    137       POTENTIAL.
FT   DOMAIN      138    147       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   147 AA;  16779 MW;  359EE741034C34E8 CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 147;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 LPLLLLL 21
              |||||||
Db         11 LPLLLLL 17


RESULT 15
RMP3_HUMAN
ID   RMP3_HUMAN     STANDARD;      PRT;   148 AA.
AC   O60896;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Receptor activity-modifying protein 3 precursor (CRLR activity-
DE   modifying-protein 3) (Calcitonin-receptor-like receptor-activity-
DE   modifying-protein 3).
GN   RAMP3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC   TISSUE=Brain;
RX   MEDLINE=98282119; PubMed=9620797;
RA   McLatchie L.M., Fraser N.J., Main M.J., Wise A., Brown J.,
RA   Thompson N., Solari R., Lee M.G., Foord S.M.;
RT   "RAMPs regulate the transport and ligand specificity of the
RT   calcitonin-receptor-like receptor.";
RL   Nature 393:333-339(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT   "cDNA clones of human proteins involved in signal transduction
RT   sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE OF 21-148 FROM N.A.
RA   Walker C., Bauer C., Smith R.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Required to transport calcitonin-receptor-like receptor
CC       (CRLR) to the plasma membrane.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Strongly expressed in lung, breast, immune
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CC       system and fetal tissues.
CC   -!- SIMILARITY: Belongs to the RAMP family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ001016; CAA04474.1; -.
DR   EMBL; AY265459; AAP23300.1; -.
DR   EMBL; BC022304; AAH22304.1; -.
DR   EMBL; AC004844; -; NOT_ANNOTATED_CDS.
DR   Genew; HGNC:9845; RAMP3.
DR   MIM; 605155; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005764; C:lysosome; TAS.
DR   GO; GO:0015031; P:protein transport; TAS.
DR   GO; GO:0006898; P:receptor mediated endocytosis; TAS.
DR   InterPro; IPR006985; RAMP.
DR   Pfam; PF04901; RAMP; 1.
KW   Signal; Transmembrane; Transport; Receptor.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    148       RECEPTOR ACTIVITY-MODIFYING PROTEIN 3.
FT   DOMAIN       24    118       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    119    138       POTENTIAL.
FT   DOMAIN      139    148       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   148 AA;  16518 MW;  EEEE312496EF513C CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 148;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 LPLLLLL 21
              |||||||
Db         12 LPLLLLL 18


Search completed: February 27, 2004, 19:37:56
Job time : 23 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 29, 2004, 08:16:48 ; Search time 69 Seconds
(without alignments)
1385.536 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 303
Sequence: 1 MGSGGDSLLGGRGSLPLLLL.....SGPRLPREARELRGQRRNTG 303

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	148	48.8	1007	4	Q8WZ75	Q8wz75 homo sapien
2	120	39.6	792	4	Q96JV6	Q96jv6 homo sapien
3	69	22.8	702	4	Q8TEG1	Q8teg1 homo sapien
4	27	8.9	961	11	Q80W87	Q80w87 rattus norv
5	27	8.9	1016	11	Q8C310	Q8c310 mus musculu
6	10	3.3	129	11	Q8VBY7	Q8vby7 mus musculu
7	10	3.3	424	11	Q8C6W0	Q8c6w0 mus musculu
8	10	3.3	1150	11	Q8BS24	Q8bs24 mus musculu
9	10	3.3	1209	11	P70232	P70232 mus musculu
10	9	3.0	362	9	Q8LTT9	Q8ltt9 bacteriopha
11	8	2.6	72	16	Q8YGC5	Q8ygc5 brucella me
12	8	2.6	123	4	Q96RL5	Q96rl5 homo sapien
13	8	2.6	189	4	Q8WU39	Q8wu39 homo sapien
14	8	2.6	205	6	Q7YRG8	Q7yrg8 cebus albif
15	8	2.6	205	11	Q810Z2	Q810z2 mus musculu
16	8	2.6	216	11	Q9CST8	Q9cst8 mus musculu
17	8	2.6	227	4	Q9UKJ0	Q9ukj0 homo sapien
18	8	2.6	233	16	Q9CHT7	Q9cht7 lactococcus
19	8	2.6	271	4	Q9HBS0	Q9hbs0 homo sapien
20	8	2.6	305	16	Q89UQ6	Q89uq6 bradyrhizob
21	8	2.6	326	10	P93680	P93680 persea amer
22	8	2.6	353	4	Q86XY3	Q86xy3 homo sapien
23	8	2.6	353	16	Q7UXV9	Q7uxv9 rhodopirell
24	8	2.6	376	2	Q93U15	Q93u15 bradyrhizob
25	8	2.6	420	5	Q8IMW5	Q8imw5 drosophila
26	8	2.6	431	10	Q9SN38	Q9sn38 arabidopsis
27	8	2.6	436	5	Q9V974	Q9v974 drosophila
28	8	2.6	453	16	Q8UHT2	Q8uht2 agrobacteri
29	8	2.6	464	11	Q9EPL5	Q9epl5 mus musculu
30	8	2.6	475	4	O75255	O75255 homo sapien
31	8	2.6	526	4	Q8NG09	Q8ng09 homo sapien
32	8	2.6	613	4	Q969P0	Q969p0 homo sapien
33	8	2.6	1501	11	Q9QW00	Q9qw00 rattus sp.
34	8	2.6	1501	11	Q7TT17	Q7tt17 mus musculu
35	8	2.6	1502	4	Q9UM81	Q9um81 homo sapien
36	8	2.6	1626	5	Q9V5X5	Q9v5x5 drosophila
37	8	2.6	1788	13	Q9IAJ0	Q9iaj0 xenopus lae
38	8	2.6	1863	11	Q64605	Q64605 rattus norv
39	8	2.6	1887	11	Q9QW67	Q9qw67 rattus sp.
40	8	2.6	1894	11	Q64487	Q64487 mus musculu
41	8	2.6	1896	13	Q9IAJ1	Q9iaj1 xenopus lae
42	8	2.6	1898	4	Q86WS0	Q86ws0 homo sapien
43	8	2.6	1898	11	Q9EQ17	Q9eq17 mus musculu
44	8	2.6	1898	11	Q64604	Q64604 r protein-t
45	8	2.6	1904	11	Q64699	Q64699 mus musculu

ALIGNMENTS

RESULT 1
Q8WZ75
ID Q8WZ75 PRELIMINARY; PRT; 1007 AA.
AC Q8WZ75;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Magic roundabout.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20530916; PubMed=11076864;
RA Huminiecki L., Bicknell R.;
RT "In silico cloning of novel endothelial-specific genes.";
RL Genome Res. 10:1796-1806(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Huminiecki L., Bicknell R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF361473; AAL31867.1; -.
DR Genew; HGNC:17985; ROBO4.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 1007 AA; 107457 MW; E43F246C59BE1415 CRC64;

Query Match 48.8%; Score 148; DB 4; Length 1007;
Best Local Similarity 100.0%; Pred. No. 8.3e-140;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114

Qy         115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174

Qy         175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202
               ||||||||||||||||||||||||||||
Db         175 GKPLALQPGRHTVSGGSLLMARAEKSDE 202


RESULT 2
Q96JV6
ID   Q96JV6      PRELIMINARY;      PRT;   792 AA.
AC   Q96JV6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein FLJ14946.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA   Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA   Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA   Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK027852; BAB55411.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein; Immunoglobulin domain.
SQ   SEQUENCE   792 AA;  85419 MW;  FC6DC05275B7B234 CRC64;

  Query Match             39.6%;  Score 120;  DB 4;  Length 792;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-111;
  Matches  120;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          55 ASGQPPPTIRWLLNGQPLSMVPPDPHHLLPDGTLLLLQPPARGHAHDGQALSTDLGVYTC 114

Qy         115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         115 EASNRLGTAVSRGARLSVAVLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKD 174


RESULT 3
Q8TEG1
ID   Q8TEG1      PRELIMINARY;      PRT;   702 AA.
AC   Q8TEG1;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   FLJ00236 protein (Fragment).
GN   FLJ00236.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
RT   "The nucleotide sequence of a long cDNA clone isolated from human
RT   spleen.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK074163; BAB84989.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain.
FT   NON_TER       1       1
SQ   SEQUENCE   702 AA;  75340 MW;  D668FEE4BCAFDCC6 CRC64;

  Query Match             22.8%;  Score 69;  DB 4;  Length 702;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-60;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         134 VLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLL 193
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          24 VLREDFQIQPRDMVAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLL 83

Qy         194 MARAEKSDE 202
               |||||||||
Db          84 MARAEKSDE 92


RESULT 4
Q80W87
ID   Q80W87      PRELIMINARY;      PRT;   961 AA.
AC   Q80W87;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   ROBO4.
GN   ROBO4.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Roberts K.G., Stewart L.M.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY277635; AAP32918.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR005829; Sug_transporter.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
SQ   SEQUENCE   961 AA;  102579 MW;  1D21E7D4B611899F CRC64;

  Query Match             8.9%;  Score 27;  DB 11;  Length 961;
```

Best Local Similarity 100.0%; Pred. No. 6e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        109 LGVYTCEASNRLGTAVSRGARLSVAVL 135
              |||||||||||||||||||||||||||
Db        120 LGVYTCEASNRLGTAVSRGARLSVAVL 146
```

RESULT 5
Q8C310
ID Q8C310 PRELIMINARY; PRT; 1016 AA.
AC Q8C310;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to MAGIC ROUNDABOUT.
GN ROBO4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK087355; BAC39850.1; -.
DR PIR; PT0635; PT0696.
DR PIR; PT0649; PT0712.
DR MGD; MGI:1921394; Robo4.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGc2; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 1016 AA; 108461 MW; DE70683C63AECD8E CRC64;

Query Match 8.9%; Score 27; DB 11; Length 1016;
Best Local Similarity 100.0%; Pred. No. 6.3e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        109 LGVYTCEASNRLGTAVSRGARLSVAVL 135
              |||||||||||||||||||||||||||
Db        120 LGVYTCEASNRLGTAVSRGARLSVAVL 146
```

RESULT 6
Q8VBY7
ID Q8VBY7 PRELIMINARY; PRT; 129 AA.
AC Q8VBY7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Close homolog of L1 precursor (Fragment).
GN CHL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129Sv;
RA Montag-Sallaz M.;
RT "Mice deficient for the close homolog of L1 (Chl1) display NCAM180
RT mRNA upregulation, abnormal hippocampal mossy fiber connectivity, and
RT altered exploratory behaviour.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ319655; CAC88131.1; -.
DR EMBL; AJ319656; CAC88131.1; JOINED.
DR EMBL; AJ319657; CAC88131.1; JOINED.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 >30 POTENTIAL.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14435 MW; FBF1A5436F9371D2 CRC64;

Query Match 3.3%; Score 10; DB 11; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        116 ASNRLGTAVS 125
              ||||||||||
Db        111 ASNRLGTAVS 120
```

RESULT 7
Q8C6W0
ID Q8C6W0 PRELIMINARY; PRT; 424 AA.
AC Q8C6W0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Close homolog of L1 (Fragment).
GN CHL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK053039; BAC35247.1; -.
DR MGD; MGI:1098266; Chl1.
DR GO; GO:0007411; P:axon guidance; IMP.
DR GO; GO:0007610; P:behavior; IMP.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00408; IGc2; 3.
DR PROSITE; PS50835; IG_LIKE; 4.
FT NON_TER 424 424
SQ SEQUENCE 424 AA; 47566 MW; C02AC0BEF5B5805C CRC64;

Query Match 3.3%; Score 10; DB 11; Length 424;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        116 ASNRLGTAVS 125
              ||||||||||
Db        111 ASNRLGTAVS 120
```

RESULT 8
Q8BS24
ID Q8BS24 PRELIMINARY; PRT; 1150 AA.
AC Q8BS24;

```
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Close homolog of L1.
GN   CHL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK040765; BAC30699.1; -.
DR   MGD; MGI:1098266; Chl1.
DR   GO; GO:0007411; P:axon guidance; IMP.
DR   GO; GO:0007610; P:behavior; IMP.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 4.
DR   Pfam; PF00047; ig; 6.
DR   SMART; SM00060; FN3; 4.
DR   SMART; SM00409; IG; 5.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 6.
SQ   SEQUENCE   1150 AA;  129000 MW;  6CF6C082529C7A99 CRC64;

  Query Match             3.3%;  Score 10;  DB 11;  Length 1150;
  Best Local Similarity   100.0%;  Pred. No. 0.95;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        116 ASNRLGTAVS 125
              ||||||||||
Db        111 ASNRLGTAVS 120


RESULT 9
P70232
ID   P70232      PRELIMINARY;      PRT;  1209 AA.
AC   P70232;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   L1-like protein.
GN   CHL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Holm J., Hillenbrand R., Steuber V., Bartsch U., Moos M., Luebbert H.,
RA   Montag D., Schachner M.;
RT   "Structural features of a close homolog of L1 (CHL1) in the mouse: a
RT   novel member of the L1 family of neural recognition molecules.";
RL   Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X94310; CAA63972.1; -.
DR   PIR; T42718; T42718.
DR   HSSP; P20241; 1CFB.
DR   MGD; MGI:1098266; Chl1.
DR   GO; GO:0007411; P:axon guidance; IMP.
DR   GO; GO:0007610; P:behavior; IMP.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 4.
DR   Pfam; PF00047; ig; 6.
DR   SMART; SM00060; FN3; 4.
DR   SMART; SM00408; IGc2; 3.
DR   PROSITE; PS50835; IG_LIKE; 6.
KW   Immunoglobulin domain.
SQ   SEQUENCE   1209 AA;  134929 MW;  331F5849AE776226 CRC64;

  Query Match             3.3%;  Score 10;  DB 11;  Length 1209;
  Best Local Similarity   100.0%;  Pred. No. 0.99;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        116 ASNRLGTAVS 125
              ||||||||||
Db        111 ASNRLGTAVS 120


RESULT 10
Q8LTT9
ID   Q8LTT9      PRELIMINARY;      PRT;  362 AA.
AC   Q8LTT9;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   DNA primase (Fragment).
OS   Bacteriophage P4.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX   NCBI_TaxID=10680;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=3937;
RA   Franza T., Michaud-Soret I., Piquerel P., Expert D.;
RT   "Coupling of iron assimilation and pectinolysis in Erwinia
RT   chrysanthemi.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF509493; AAM28906.1; -.
DR   GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR   GO; GO:0005488; F:binding; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR001993; Mitoch_carrier.
DR   PROSITE; PS00215; MITOCH_CARRIER; 1.
FT   NON_TER       1      1
FT   NON_TER     362    362
SQ   SEQUENCE   362 AA;  38936 MW;  CF20E6BDAC873710 CRC64;

  Query Match             3.0%;  Score 9;  DB 9;  Length 362;
  Best Local Similarity   100.0%;  Pred. No. 3.3;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         82 LLPDGTLLL 90
              |||||||||
Db        106 LLPDGTLLL 114


RESULT 11
Q8YGC5
ID   Q8YGC5      PRELIMINARY;      PRT;  72 AA.
AC   Q8YGC5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical membrane associated protein BMEI1234.
GN   BMEI1234.
OS   Brucella melitensis.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Brucellaceae; Brucella.
OX   NCBI_TaxID=29459;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=16M / ATCC 23456 / Biotype 1;
RX   MEDLINE=20020109; PubMed=11756688;
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RA   DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA   Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA   Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA   Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA   Haselkorn R., Kyrpides N., Overbeek R.;
RT   "The genome sequence of the facultative intracellular pathogen
RT   Brucella melitensis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR   EMBL; AE009562; AAL52415.1; -.
DR   PIR; AD3406; AD3406.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   72 AA;  8311 MW;  D064085089A5AE04 CRC64;

  Query Match             2.6%;  Score 8;  DB 16;  Length 72;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GSLPLLLL 20
              ||||||||
Db         44 GSLPLLLL 51


RESULT 12
Q96RL5
ID   Q96RL5      PRELIMINARY;      PRT;   123 AA.
AC   Q96RL5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Proapoptotic caspase adaptor protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21369886; PubMed=11350957;
RA   Bonfoco E., Li E., Kolbinger F., Cooper N.R.;
RT   "Characterization of a novel proapoptotic caspase-2- and caspase-9-
RT   binding protein.";
RL   J. Biol. Chem. 276:29242-29250(2001).
DR   EMBL; AF338109; AAK84085.1; -.
SQ   SEQUENCE   123 AA;  13066 MW;  C21A354CE08A95CB CRC64;

  Query Match             2.6%;  Score 8;  DB 4;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 SLPLLLLL 21
              ||||||||
Db          4 SLPLLLLL 11


RESULT 13
Q8WU39
ID   Q8WU39      PRELIMINARY;      PRT;   189 AA.
AC   Q8WU39;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to RIKEN cDNA 2010001M09 gene.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tonsil;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC021275; AAH21275.1; -.
DR   InterPro; IPR000886; ER_target_S.
DR   PROSITE; PS00014; ER_TARGET; 1.
SQ   SEQUENCE   189 AA;  20694 MW;  C71AED212D3393D3 CRC64;

  Query Match             2.6%;  Score 8;  DB 4;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 SLPLLLLL 21
              ||||||||
Db          4 SLPLLLLL 11


RESULT 14
Q7YRG8
ID   Q7YRG8      PRELIMINARY;      PRT;   205 AA.
AC   Q7YRG8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   LOC122650.
OS   Cebus albifrons (White-fronted capuchin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
OX   NCBI_TaxID=9514;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Devor E.J., Moffat-Wilson K.A.;
RT   "LOC122650 on chromosome 14q11.2 is related to the RNase A superfamily
RT   and contains a unique amino-terminal pre-protein-like domain.";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY330198; AAQ01508.1; -.
SQ   SEQUENCE   205 AA;  24294 MW;  DBFC3217F7A070D0 CRC64;

  Query Match             2.6%;  Score 8;  DB 6;  Length 205;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 SLPLLLLL 21
              ||||||||
Db          8 SLPLLLLL 15


RESULT 15
Q810Z2
ID   Q810Z2      PRELIMINARY;      PRT;   205 AA.
AC   Q810Z2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Collagenase-like B (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SVJ;
RA   Brathwaite M., Waeltz P., Nagaraja R.;
RT   "Genomic Sequence Analysis in the Mouse t-complex Region.";
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY211543; AAO37584.1; -.
DR   GO; GO:0005578; C:extracellular matrix; IEA.
DR   GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR006026; Peptidase_M.
DR   InterPro; IPR001818; Pept_M10A_M12B.
DR   Pfam; PF00413; Peptidase_M10; 1.
DR   Pfam; PF03933; Peptidase_M10_N; 1.
DR   PRINTS; PR00138; MATRIXIN.
DR   SMART; SM00235; ZnMc; 1.
DR   PROSITE; PS00546; CYSTEINE_SWITCH; 1.
FT   NON_TER     205    205
SQ   SEQUENCE   205 AA;  23403 MW;  DBD1E974E8769643 CRC64;
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Query Match 2.6%; Score 8; DB 11; Length 205;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         14 SLPLLLLL 21
              ||||||||
Db          3 SLPLLLLL 10
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Search completed: February 29, 2004, 08:19:08
Job time : 75 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 29, 2004, 22:51:24 ; Search time 2913 Seconds
(without alignments)
3106.159 Million cell updates/sec

Title: US-10-047-021-86
Perfect score: 303
Sequence: 1 MGSGGDSLLGGRGSLPLLLL.....SGPRLPREARELRGQRRNTG 303

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Word size: 1

Total number of hits satisfying chosen parameters: 55025477

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US10047021/runat_20022004_154122_4533/app_query.fasta_1.455
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST:*
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6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
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12: gb_est3:*
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14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	202	66.7	826	14	CB994099	CB994099 AGENCOURT
2	202	66.7	860	14	CB996189	CB996189 AGENCOURT
3	202	66.7	885	14	CF994298	CF994298 AGENCOURT
4	182	60.1	803	14	CB997292	CB997292 AGENCOURT
5	176	58.1	688	14	CB961818	CB961818 AGENCOURT
6	176	58.1	798	14	CB961529	CB961529 AGENCOURT
7	173	57.1	558	9	AL602474	AL602474 DKFZp686O
8	148	48.8	1019	12	BM921911	BM921911 AGENCOURT
9	148	48.8	3758	11	BC039602	BC039602 Homo sapi
10	133	43.9	771	14	CB959649	CB959649 AGENCOURT
11	133	43.9	1230	12	BM906521	BM906521 AGENCOURT
12	131	43.2	941	13	BQ890126	BQ890126 AGENCOURT
13	126	41.6	1201	9	AL553360	AL553360 AL553360
14	123	40.6	1028	14	CF994063	CF994063 AGENCOURT
15	110	36.3	797	14	CB961002	CB961002 AGENCOURT
16	109	36.0	502	13	BX474842	BX474842 DKFZp686M
17	107	35.3	610	12	BG745318	BG745318 602723637
18	97	32.0	532	13	BX475138	BX475138 DKFZp686O
19	93	30.7	729	12	BI762862	BI762862 603048384
20	88	29.0	501	13	BX474746	BX474746 DKFZp686B
21	85	28.1	1087	12	BM914311	BM914311 AGENCOURT
22	79	26.1	438	13	BX475177	BX475177 DKFZp686F
23	71	23.4	922	13	BX418142	BX418142 BX418142
24	70	23.1	424	13	BX475172	BX475172 DKFZp686E
25	70	23.1	426	13	BX492967	BX492967 DKFZp781F
26	70	23.1	526	14	CA394658	CA394658 cs54c07.y
c 27	63	20.8	344	9	AA577940	AA577940 nl20d01.s
28	63	20.8	450	9	AL039859	AL039859 DKFZp434E
29	51	16.8	1257	14	CB993951	CB993951 AGENCOURT
30	38	12.5	555	12	BI836220	BI836220 603085778
31	35	11.6	570	10	BE233526	BE233526 139756 MA
32	32	10.6	215	13	BX474950	BX474950 DKFZp686I
33	28	9.2	543	29	CE728068	CE728068 tigr-gss-
34	27	8.9	441	13	BY285423	BY285423 BY285423
35	27	8.9	455	10	BB839755	BB839755 BB839755
36	27	8.9	529	13	BX520802	BX520802 BX520802
37	27	8.9	551	9	AI116483	AI116483 ud74c06.y
38	27	8.9	557	13	BY704924	BY704924 BY704924
39	27	8.9	620	10	BB664621	BB664621 BB664621
40	27	8.9	631	10	BE376779	BE376779 601227331
41	27	8.9	655	14	CF170054	CF170054 B0821H10-
42	27	8.9	662	13	BY727209	BY727209 BY727209
43	27	8.9	3689	11	AK004723	AK004723 Mus muscu
44	27	8.9	3865	11	AK087355	AK087355 Mus muscu
45	25	8.3	264	28	BH257414	BH257414 CH230-243

ALIGNMENTS

RESULT 1
CB994099
LOCUS CB994099 826 bp mRNA linear EST 01-MAY-2003
DEFINITION AGENCOURT_13642710 NIH_MGC_148 Homo sapiens cDNA clone IMAGE:30331943 5', mRNA sequence.
ACCESSION CB994099
VERSION CB994099.1 GI:30288619
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 826)

```
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Stefan Hansson
             cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
            and advice from Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM348  row: c  column: 24
            High quality sequence stop: 637.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30331943"
                     /tissue_type="pre-eclamptic placenta"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_148"
                     /note="Organ: placenta; Vector: pBluescriptR; Site_1:
                     alI-XhoI; Site_2: BamH; Library is oligo-dT primed and
                     directionally cloned using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert
                     size 2.3 kb  and normalized to ROT 5. This is a primary
                     library enriched for  full-lenght clones and constructed
                     using the Cap-trapper method  (Carninci, in preparation).
                     Library constructed by M. Brownstein  (NIMH/NHGRI,
                     National Institutes of Health). Note: this is a NIH_MGC
                     Library."
ORIGIN

Alignment Scores:
Pred. No.:                3.18e-158       Length:         826
Score:                    202.00          Matches:        202
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              66.67%          Indels:         0
DB:                       14              Gaps:           0

US-10-047-021-86 (1-303) x CB994099 (1-826)

Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 97

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 157

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCGAGCCTCAGGCCAGCCACCT 217

Qy         61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 CCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACAC 277

Qy         81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 CACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCAC 337

Qy        101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 GATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 397

Qy        121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAG 457

Qy        141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 ATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCG 517

Qy        161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 CCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTC 577

Qy        181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 CAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGT 637

Qy        201 AspGlu 202
              ||||||
Db        638 GACGAA 643

RESULT 2
CB996189
LOCUS       CB996189                860 bp    mRNA    linear   EST 01-MAY-2003
DEFINITION  AGENCOURT_13622686 NIH_MGC_148 Homo sapiens cDNA clone
            IMAGE:30337143 5', mRNA sequence.
ACCESSION   CB996189
VERSION     CB996189.1  GI:30290709
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 860)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Stefan Hansson
             cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
            and advice from Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM361  row: l  column: 16
            High quality sequence stop: 578.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30337143"
                     /tissue_type="pre-eclamptic placenta"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_148"
                     /note="Organ: placenta; Vector: pBluescriptR; Site_1:
                     alI-XhoI; Site_2: BamH; Library is oligo-dT primed and
                     directionally cloned using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert
                     size 2.3 kb  and normalized to ROT 5. This is a primary
                     library enriched for  full-lenght clones and constructed
                     using the Cap-trapper method  (Carninci, in preparation).
                     Library constructed by M. Brownstein  (NIMH/NHGRI,
                     National Institutes of Health). Note: this is a NIH_MGC
                     Library."
ORIGIN

Alignment Scores:
Pred. No.:                3.32e-158       Length:         860
Score:                    202.00          Matches:        202
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              66.67%          Indels:         0
DB:                       14              Gaps:           0
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US-10-047-021-86 (1-303) x CB996189 (1-860)

Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
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Db         38 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 97

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 157

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCGAGCCTCAGGCCAGCCACCT 217

Qy         61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 CCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACAC 277

Qy         81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
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Db        278 CACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCAC 337

Qy        101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 GATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 397

Qy        121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAG 457

Qy        141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 ATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCG 517

Qy        161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 CCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTC 577

Qy        181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 CAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGT 637

Qy        201 AspGlu 202
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Db        638 GACGAA 643
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RESULT 3
CF994298
LOCUS       CF994298               885 bp    mRNA    linear   EST 25-NOV-2003
DEFINITION  AGENCOURT_15622355 NIH_MGC_147 Homo sapiens cDNA clone
            IMAGE:30706303 5', mRNA sequence.
ACCESSION   CF994298
VERSION     CF994298.1  GI:38510358
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 885)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Stefan Hansson
             cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
            and advice from Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM1069  row: f  column: 08
            High quality sequence stop: 642.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30706303"
                     /tissue_type="Human Placenta"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_147"
                     /note="Organ: placenta; Vector: pBluescriptR; Site_1:
                     alI-XhoI; Site_2: BamH; Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected  for average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using  the Cap-trapper method (Carninci, in
                     preparation). Library constructed  by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: This is
                     a NIH_MGC library."
ORIGIN

Alignment Scores:
Pred. No.:               3.43e-158       Length:          885
Score:                   202.00          Matches:         202
Percent Similarity:      100.00%         Conservative:    0
Best Local Similarity:   100.00%         Mismatches:      0
Query Match:             66.67%          Indels:          0
DB:                      14              Gaps:            0

US-10-047-021-86 (1-303) x CF994298 (1-885)

Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 97

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 157

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCGAGCCTCAGGCCAGCCACCT 217

Qy         61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 CCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACAC 277

Qy         81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 CACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCAC 337

Qy        101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
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Db        338 GATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 397

Qy        121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAG 457

Qy        141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
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Db        458 ATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCG 517

Qy        161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 CCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTC 577

Qy        181 GlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSer 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        578 CAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGT 637

Qy        201 AspGlu 202
              ||||||
Db        638 GACGAA 643

RESULT 4
CB997292
LOCUS       CB997292                803 bp    mRNA    linear   EST 01-MAY-2003
DEFINITION  AGENCOURT_13623935 NIH_MGC_148 Homo sapiens cDNA clone
            IMAGE:30336795 5', mRNA sequence.
ACCESSION   CB997292
VERSION     CB997292.1  GI:30291812
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 803)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Stefan Hansson
             cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
            and advice from Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM360  row: n  column: 04
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="IMAGE:30336795"
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                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_148"
                     /note="Organ: placenta; Vector: pBluescriptR; Site_1:
                     alI-XhoI; Site_2: BamH; Library is oligo-dT primed and
                     directionally cloned using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert
                     size 2.3 kb  and normalized to ROT 5. This is a primary
                     library enriched for  full-lenght clones and constructed
                     using the Cap-trapper method  (Carninci, in preparation).
                     Library constructed by M. Brownstein  (NIMH/NHGRI,
                     National Institutes of Health). Note: this is a NIH_MGC
                     Library."
ORIGIN

Alignment Scores:
Pred. No.:              1.53e-141       Length:         803
Score:                  182.00          Matches:        182
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            60.07%          Indels:         0
DB:                     14              Gaps:           0

US-10-047-021-86 (1-303) x CB997292 (1-803)

Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 97

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 157

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCGAGCCTCAGGCCAGCCACCT 217

Qy         61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 CCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACAC 277

Qy         81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
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Db        278 CACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCAC 337

Qy        101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 GATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 397

Qy        121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAG 457

Qy        141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 ATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCG 517

Qy        161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLeu 180
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Db        518 CCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCTC 577

Qy        181 GlnPro 182
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Db        578 CAGCCC 583

RESULT 5
CB961818
LOCUS       CB961818                688 bp    mRNA    linear   EST 29-APR-2003
DEFINITION  AGENCOURT_13665726 NIH_MGC_148 Homo sapiens cDNA clone
            IMAGE:30349135 5', mRNA sequence.
ACCESSION   CB961818
VERSION     CB961818.1  GI:30217935
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 688)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Stefan Hansson
             cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
            and advice from Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM392  row: p  column: 08
            High quality sequence stop: 448.
FEATURES             Location/Qualifiers
     source          1. .688
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30349135"
                     /tissue_type="pre-eclamptic placenta"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_148"
                     /note="Organ: placenta; Vector: pBluescriptR; Site_1:
                     alI-XhoI; Site_2: BamH; Library is oligo-dT primed and
                     directionally cloned using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert
```

size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-lenght clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	1.32e-136	Length:	688
Score:	176.00	Matches:	176
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	58.09%	Indels:	0
DB:	14	Gaps:	0

US-10-047-021-86 (1-303) x CB961818 (1-688)

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Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 97

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 157

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCGAGCCTCAGGCCAGCCACCT 217

Qy         61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 CCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACAC 277

Qy         81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 CACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCAC 337

Qy        101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
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Db        338 GATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 397

Qy        121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAG 457

Qy        141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 ATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCG 517

Qy        161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLys 176
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Db        518 CCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAA 565
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RESULT 6
CB961529
LOCUS CB961529 798 bp mRNA linear EST 29-APR-2003
DEFINITION AGENCOURT_13893367 NIH_MGC_148 Homo sapiens cDNA clone IMAGE:30348011 5', mRNA sequence.
ACCESSION CB961529
VERSION CB961529.1 GI:30217646
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 798)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM390 row: a column: 12
High quality sequence stop: 565.
FEATURES Location/Qualifiers
source 1. .798
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30348011"
/tissue_type="pre-eclamptic placenta"
/lab_host="DH10B TonA"
/clone_lib="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site_1: alI-XhoI; Site_2: BamH; Library is oligo-dT primed and directionally cloned using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-lenght clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:

Pred. No.:	1.55e-136	Length:	798
Score:	176.00	Matches:	176
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	58.09%	Indels:	0
DB:	14	Gaps:	0

US-10-047-021-86 (1-303) x CB961529 (1-798)

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Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 97

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 157

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCGAGCCTCAGGCCAGCCACCT 217

Qy         61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 CCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACAC 277

Qy         81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 CACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCAC 337

Qy        101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 GATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 397

Qy        121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAG 457

Qy        141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 ATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCG 517

Qy        161 ProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLys 176
```

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                 ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 CCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAA 565

RESULT 7
AL602474
LOCUS       AL602474                558 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp686O1413_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686O1413 5', mRNA sequence.
ACCESSION   AL602474
VERSION     AL602474.1  GI:15165980
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 558)
  AUTHORS   Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.
  TITLE     EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686O1413) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .558
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686O1413"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="686 (synonym: hlcc3)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN

Alignment Scores:
Pred. No.:              3.34e-134      Length:         558
Score:                  173.00         Matches:        173
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            57.10%         Indels:         0
DB:                     9              Gaps:           0

US-10-047-021-86 (1-303) x AL602474 (1-558)

Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 99

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCTTAGTCCACCCCCAGGAC 159

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCGAGCCTCAGGCCAGCCACCT 219

Qy         61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACAC 279

Qy         81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        280 CACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCAC 339

Qy        101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 GATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 399

Qy        121 GlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 GGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAG 459

Qy        141 IleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPro 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 ATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCCG 519

Qy        161 ProTrpGlyHisProGluProThrValSerTrpTrpLys 173
              |||||||||||||||||||||||||||||||||||||
Db        520 CCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAA 558

RESULT 8
BM921911
LOCUS       BM921911                1019 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6706908 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753515
            5', mRNA sequence.
ACCESSION   BM921911
VERSION     BM921911.1  GI:19372290
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1019)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12789  row: g  column: 20
            High quality sequence stop: 697.
FEATURES             Location/Qualifiers
     source          1. .1019
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5753515"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_115"
                     /note="Organ: pooled brain, lung, testis; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 6 male brains, age range 23-27; 1
                     male lung, age 27; and 1 male testis, age 69.  Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon  cloning).  Average insert size 1.8 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was  constructed by C.
                     Gruber (Invitrogen).  Research Genetics tracking  code
                     021. Note: this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              4.79e-113      Length:         1019
Score:                  148.00         Matches:        211
Percent Similarity:     99.06%         Conservative:   0
Best Local Similarity:  99.06%         Mismatches:     1
Query Match:            48.84%         Indels:         2
DB:                     12             Gaps:           0
```

US-10-047-021-86 (1-303) x BM921911 (1-1019)

```
Qy         55 AlaSerGlyGlnProProProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMet 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 GCCTCAGGCCAGCCACCTCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATG 135

Qy         75 ValProProAspProHisHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProPro 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GTGCCCCCAGACCCACACCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCT 195

Qy         95 AlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCys 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GCCCGGGGACATGCCCACGATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGT 255

Qy        115 GluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaVal 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTC 315

Qy        135 LeuArgGluAspPheGlnIleGlnProArgAspMetValAlaValValGlyGluGlnPhe 154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 CTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTT 375

Qy        155 ThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTrpLysAsp 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 ACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGAT 435

Qy        175 GlyLysProLeuAlaLeuGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMet 194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GGGAAACCCCTGGCCCTCCAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATG 495

Qy        195 AlaArgAlaGluLysSerAspGlu***-ThrTyrMetCysValAlaThrAsnSerAlaGl 214
              |||||||||||||||||||||||    |||||||||||||||||||||||||||||||
Db        496 GCAAGAGCAGAGAAGAGTGACGAAGG-GACCTACATGTGTGTGGCCACCAACAGCGCAGG 554

Qy        214 yHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGlnAspTyrThrGluPr 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 ACATAGGGAGAGCCGCGCAGCCCGGGTTTCCATCCAGGAGCCCCAGGACTACACGGAGCC 614

Qy        234 oValGluLeuLeuAlaValArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspPr 254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        615 TGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAAATGTGACACTGCTGAACCCGGATCC 674

Qy        254 oAlaGluGlyProLysProArgProAlaValTrpLeu 266
              ||||||||||||||||||||||||||||||||||||
Db        675 TGCAGAGGGCCCCAAGCCTAGACCGGCGGTGTGGCTC 711
```

RESULT 9
BC039602

```
LOCUS       BC039602               3758 bp    mRNA    linear   HTC 06-NOV-2002
DEFINITION  Homo sapiens, Similar to roundabout homolog 4, magic roundabout
            (Drosophila), clone IMAGE:5590503, mRNA.
ACCESSION   BC039602
VERSION     BC039602.1  GI:24660430
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3758)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 84 Row: i Column: 5
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis, GenomeScan gene prediction
            This clone has the following problem: frame shifted.
FEATURES              Location/Qualifiers
     source           1. .3758
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:5590503"
                      /tissue_type="Ovary, pooled from 3 adults"
                      /clone_lib="NIH_MGC_125"
                      /lab_host="DH10B"
                      /note="Vector: pCMV-SPORT6"
ORIGIN
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```
Alignment Scores:
Pred. No.:                2.01e-112       Length:          3758
Score:                    148.00          Matches:         264
Percent Similarity:       98.51%          Conservative:    0
Best Local Similarity:    98.51%          Mismatches:      2
Query Match:              48.84%          Indels:          4
DB:                       11              Gaps:            0
```

US-10-047-021-86 (1-303) x BC039602 (1-3758)

```
Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 88

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 148

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
              ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db        149 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACC 207

Qy         60 oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 TCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACA 267

Qy         80 sHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 CCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCA 327

Qy        100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 CGATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCT 387

Qy        120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TGGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCA 447

Qy        140 nIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 GATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCC 507

Qy        160 oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCT 567

Qy        180 uGlnProGlyArgHisThrValSerGlyGlySerLeuLeuMetAlaArgAlaGluLysSe 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 CCAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAG 627
```

```
Qy        200 rAspGlu***-ThrTyrMetCysValAlaThrAsnSerAlaGlyHisArgGluSerArgA 220
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 TGACGAAGG-GACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCG 686

Qy        220 laAlaArgValSerIleGlnGluProGlnAspTyrThrGluProValGluLeuLeuAlaV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 CAGCCCGGGTTTCCATCCAGGAGCCCCAGGACTACACGGAGCCTGTGGAGCTTCTGGCTG 746

Qy        240 alArgIleGlnLeuGluAsnValThrLeuLeuAsnProAspProAlaGluGlyProLysP 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 TGCGAATTCAGCTGGAAAATGTGACACTGCTGAACCCGGATCCTGCAGAGGGCCCCAAGC 806

Qy        260 roArgProAlaValTrpLeu 266
              ||||||||||||||||||
Db        807 CTAGACCGGCGGTGTGGCTC 826

RESULT 10
CB959649
LOCUS       CB959649                771 bp    mRNA    linear   EST 29-APR-2003
DEFINITION  AGENCOURT_13893577 NIH_MGC_147 Homo sapiens cDNA clone
            IMAGE:30344820 5', mRNA sequence.
ACCESSION   CB959649
VERSION     CB959649.1  GI:30215765
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 771)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Stefan Hansson
             cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
            and advice from Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM381  row: l  column: 13
            High quality sequence stop: 628.
FEATURES             Location/Qualifiers
     source          1. .771
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30344820"
                     /tissue_type="Human Placenta"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_147"
                     /note="Organ: placenta; Vector: pBluescriptR; Site_1:
                     alI-XhoI; Site_2: BamH; Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTTVN-3', size-selected  for average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using  the Cap-trapper method (Carninci, in
                     preparation). Library constructed  by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: This is
                     a NIH_MGC library."
ORIGIN

Alignment Scores:
Pred. No.:              1.17e-100       Length:         771
Score:                  133.00          Matches:        186
Percent Similarity:     98.94%          Conservative:   0
Best Local Similarity:  98.94%          Mismatches:     1
Query Match:            43.89%          Indels:         2
DB:                     14              Gaps:           0

US-10-047-021-86 (1-303) x CB959649 (1-771)
```

```
Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 125

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 185

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        186 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACC 244

Qy         60 oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 TCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACA 304

Qy         80 sHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 CCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCA 364

Qy        100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 CGATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCT 424

Qy        120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 TGGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCA 484

Qy        140 nIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 GATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCC 544

Qy        160 oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 GCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCT 604

Qy        180 uGlnProGlyArgHisThrVal 187
              |||||||||||||||||||
Db        605 CCAGCCCGGAAGGCACACAGTG 626

RESULT 11
BM906521
LOCUS       BM906521                1230 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6620212 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590503
            5', mRNA sequence.
ACCESSION   BM906521
VERSION     BM906521.1  GI:19356900
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1230)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12364  row: o  column: 16
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .1230
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
```

/clone="IMAGE:5590503"
/lab_host="DH10B"
/clone_lib="NIH_MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

ORIGIN

Alignment Scores:

Pred. No.:	1.96e-100	Length:	1230
Score:	133.00	Matches:	186
Percent Similarity:	98.94%	Conservative:	0
Best Local Similarity:	98.94%	Mismatches:	1
Query Match:	43.89%	Indels:	2
DB:	12	Gaps:	0

US-10-047-021-86 (1-303) x BM906521 (1-1230)

```
Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 94

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 154

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
              |||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        155 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACC 213

Qy         60 oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACA 273

Qy         80 sHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 CCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCA 333

Qy        100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CGATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCT 393

Qy        120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 TGGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCA 453

Qy        140 nIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 GATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCC 513

Qy        160 oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCT 573

Qy        180 uGlnProGlyArgHisThrVal 187
              |||||||||||||||||||
Db        574 CCAGCCCGGAAGGCACACAGTG 595
```

RESULT 12
BQ890126
LOCUS BQ890126 941 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT_7982449 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:6186214 5', mRNA sequence.
ACCESSION BQ890126
VERSION BQ890126.1 GI:22282140
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 941)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13578 row: d column: 23
High quality sequence start: 6
High quality sequence stop: 612.
FEATURES Location/Qualifiers
source 1. .941
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6186214"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupski_dorsal_root_ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	6.82e-99	Length:	941
Score:	131.00	Matches:	184
Percent Similarity:	98.92%	Conservative:	0
Best Local Similarity:	98.92%	Mismatches:	1
Query Match:	43.23%	Indels:	2
DB:	13	Gaps:	0

US-10-047-021-86 (1-303) x BQ890126 (1-941)

```
Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         53 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 112

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 172

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60
              |||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
Db        173 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACC 231

Qy         60 oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 TCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACA 291

Qy         80 sHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 CCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCA 351

Qy        100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLe 120
```

```
Db        352 CGATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCT 411

Qy        120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140

Db        412 TGGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCA 471

Qy        140 nIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPr 160

Db        472 GATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCC 531

Qy        160 oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLe 180

Db        532 GCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCT 591

Qy        180 uGlnProGlyArgHis 185

Db        592 CCAGCCCGGAAGGCAC 607
```

```
RESULT 13
AL553360
LOCUS       AL553360                1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL553360 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI075YP13 5-PRIME, mRNA sequence.
ACCESSION   AL553360
VERSION     AL553360.2  GI:31275174
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12893123.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6206.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI075CH07QP1&cluster=6206.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI075CH07QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI075YP13"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Alignment Scores:
Pred. No.:                1.33e-94        Length:          1201
Score:                    126.00          Matches:         179
Percent Similarity:       98.90%          Conservative:    0
Best Local Similarity:    98.90%          Mismatches:      1
Query Match:              41.58%          Indels:          2
DB:                       9               Gaps:            0

US-10-047-021-86 (1-303) x AL553360 (1-1201)

Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
```

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Db         81 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 140

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40

Db        141 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 200

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArg-AlaSerGlyGlnProPr 60

Db        201 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCA-AGCCTCAGGCCAGCCACC 259

Qy         60 oProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHi 80

Db        260 TCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACA 319

Qy         80 sHisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHi 100

Db        320 CCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCA 379

Qy        100 sAspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLe 120

Db        380 CGATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCT 439

Qy        120 uGlyThrAlaValSerArgGlyAlaArgLeuSerValAlaValLeuArgGluAspPheGl 140

Db        440 TGGCACGGCAGTTAGCAGAGGCGCTCGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCA 499

Qy        140 nIleGlnProArgAspMetValAlaValValGlyGluGlnPheThrLeuGluCysGlyPr 160

Db        500 GATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAGTTTACTCTGGAATGTGGGCC 559

Qy        160 oProTrpGlyHisProGluProThrValSerTrpTrpLysAspGlyLysProLeuAlaLe 180

Db        560 GCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTGGCCCT 619

Qy        180 u 180

Db        620 C 620
```

```
RESULT 14
CF994063
LOCUS       CF994063                1028 bp    mRNA    linear   EST 25-NOV-2003
DEFINITION  AGENCOURT_15622361 NIH_MGC_147 Homo sapiens cDNA clone
            IMAGE:30519942 5', mRNA sequence.
ACCESSION   CF994063
VERSION     CF994063.1  GI:38510123
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1028)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Stefan Hansson
             cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
            and advice from Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM592  row: e  column: 07
            High quality sequence stop: 411.
FEATURES             Location/Qualifiers
     source          1. .1028
                     /organism="Homo sapiens"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30519942"
/tissue_type="Human Placenta"
/lab_host="DH10B TonA"
/clone_lib="NIH_MGC_147"
/note="Organ: placenta; Vector: pBluescriptR; Site_1: alI-XhoI; Site_2: BamH; Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: This is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.:	3.58e-92	Length:	1028
Score:	123.00	Matches:	123
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	40.59%	Indels:	0
DB:	14	Gaps:	0

US-10-047-021-86 (1-303) x CF994063 (1-1028)

```
Qy          1 MetGlySerGlyGlyAspSerLeuLeuGlyGlyArgGlySerLeuProLeuLeuLeuLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38 ATGGGCTCTGGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTG 97

Qy         21 LeuIleMetGlyGlyMetAlaGlnAspSerProProGlnIleLeuValHisProGlnAsp 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CTCATCATGGGAGGCATGGCTCAGGACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGAC 157

Qy         41 GlnLeuPheGlnGlyProGlyProAlaArgMetSerCysArgAlaSerGlyGlnProPro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 CAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGCCGAGCCTCAGGCCAGCCACCT 217

Qy         61 ProThrIleArgTrpLeuLeuAsnGlyGlnProLeuSerMetValProProAspProHis 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 CCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGACCCACAC 277

Qy         81 HisLeuLeuProAspGlyThrLeuLeuLeuLeuGlnProProAlaArgGlyHisAlaHis 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 CACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCAC 337

Qy        101 AspGlyGlnAlaLeuSerThrAspLeuGlyValTyrThrCysGluAlaSerAsnArgLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 GATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTT 397

Qy        121 GlyThrAla 123
              ||||||||
Db        398 GGCACGGCA 406
```

RESULT 15
CB961002

```
LOCUS       CB961002                797 bp    mRNA    linear   EST 29-APR-2003
DEFINITION  AGENCOURT_13761727 NIH_MGC_147 Homo sapiens cDNA clone
            IMAGE:30343790 5', mRNA sequence.
ACCESSION   CB961002
VERSION     CB961002.1  GI:30217119
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 797)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Stefan Hansson
            cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
            and advice from Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM379  row: a  column: 15
            High quality sequence stop: 475.
FEATURES             Location/Qualifiers
     source          1. .797
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30343790"
                     /tissue_type="Human Placenta"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_147"
                     /note="Organ: placenta; Vector: pBluescriptR; Site_1:
                     alI-XhoI; Site_2: BamH; Oligo-dT primed using primer
                     5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein
                     (NIMH/NHGRI, National Institutes of Health). Note: This is
                     a NIH_MGC library."
ORIGIN
```

Alignment Scores:

Pred. No.:	1.93e-81	Length:	797
Score:	110.00	Matches:	152
Percent Similarity:	98.70%	Conservative:	0
Best Local Similarity:	98.70%	Mismatches:	1
Query Match:	36.30%	Indels:	2
DB:	14	Gaps:	0

US-10-047-021-86 (1-303) x CB961002 (1-797)

```
Qy         93 ProProAlaArgGlyHisAlaHisAspGlyGlnAlaLeuSerThrAspLeuGlyValTyr 112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 CCCCCTGCCCGGGGACATGCCCACGATGGCCAGGCCCTGTCCACAGACCTGGGTGTCTAC 167

Qy        113 ThrCysGluAlaSerAsnArgLeuGlyThrAlaValSerArgGlyAlaArgLeuSerVal 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 ACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGCGCTCGGCTGTCTGTG 227

Qy        133 AlaValLeuArgGluAspPheGlnIleGlnProArgAspMetValAlaValValGlyGlu 152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 GCTGTCCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAG 287

Qy        153 GlnPheThrLeuGluCysGlyProProTrpGlyHisProGluProThrValSerTrpTrp 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 CAGTTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGG 347

Qy        173 LysAspGlyLysProLeuAlaLeuGlnProGlyArgHisThrValSerGlyGlySerLeu 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 AAAGATGGGAAACCCCTGGCCCTCCAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTG 407

Qy        193 LeuMetAlaArgAlaGluLysSerAspGlu***-ThrTyrMetCysValAlaThrAsnSe 212
              |||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db        408 CTGATGGCAAGAGCAGAGAAGAGTGACGAAGG-GACCTACATGTGTGTGGCCACCAACAG 466

Qy        212 rAlaGlyHisArgGluSerArgAlaAlaArgValSerIleGlnGluProGlnAspTyrTh 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 CGCAGGACACAGGGAGAGCCGCGCAGCCCGGGTTTCCATCCAGGAGCCCCAGGACTACAC 526

Qy        232 rGluProValGluLeuLeuAlaValArgIleGlnLeuGlu 245
              |||||||||||||||||||||||||||||||||||||||
Db        527 GGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAA 566
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Search completed: March 1, 2004, 09:17:43
Job time : 2926 secs